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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 25, 2004, 09:15:20 ; Search time 53.5 Seconds
(without alignments)
5365.762 Million cell updates/sec

Title: US-09-914-324A-3

Sequence: 1 cccaataatgcgcgcagcagat.....aaagtcacgttcgattcgcg 508

Scoring table:

BIOSIM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Rgapop 6.0, Rgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPRO.spool/p/US09914324/runat.25032004.090846.8708/app.query.fasta_1.647
-DB-A=Geneseq.292004 -OPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNIT=bits -START=1 -END=-1 -MATRIX=blosome62 -TRANS=human40.cdi
-LIST=45 -DOCALLIG=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09914324 @CGN.1.1_81 @runat.25032004.090846.8708 -NCPU=6 -ICPU=3
-NO MAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSBLOCCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: A_Geneseq_292004:

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	64.0	108	3	AAB19160 Amino aci
2	616	64.0	108	3	AAB08813 A human c
3	616	64.0	108	3	AAG02890 Human sec
4	616	64.0	108	4	AAB47599 ROC1. 1/2
5	616	64.0	108	5	AAB24620 Human RIN
6	616	64.0	108	7	ADC02481 RING fing
7	534	55.5	108	4	ABE68080 Drosophi1
8	514.5	53.5	118	3	AAG23004 Arabidops
9	511	53.1	109	3	AAG23005 Arabidops
10	400.5	41.6	122	4	ABE66109 Drosophi1

11	385	40.0	121	3	AAB08814 A Yeast C
12	323	33.6	57	4	AAB41007 Human ORF
13	294	30.6	118	4	AAB15873 Human nov
14	294	30.6	118	6	ABU54942 Human nov
15	292	30.4	113	3	AAV06492 Human sen
16	292	30.4	113	3	AAH43295 Human ORF
17	292	30.4	131	4	AAU16332 Human nov
18	292	30.4	131	6	ABU55401 Human nov
19	291	30.2	113	2	AAV06509 Human sen
20	290.5	30.2	113	2	AAV06491 Amino aci
21	290.5	30.2	113	3	ABAB19161 Mouse sen
22	287	29.8	113	3	ABAB47600 ROC2. 1/2
23	287	29.8	113	5	AAE24621 Human RIN
24	287	29.8	113	7	ADC02483 RING fing
25	285	29.6	113	2	AAV06508 Human sen
26	283	29.4	113	2	AAV06500 Human sen
27	283	29.4	113	2	AAV06501 Human sen
28	282	29.3	113	2	AAV06496 Human sen
29	282	29.3	113	2	AAV06503 Human sen
30	282	29.3	113	2	AAV06502 Human sen
31	282	29.3	113	2	AAV06506 Human sen
32	282	29.3	113	2	AAV06495 Human sen
33	282	29.3	113	2	AAV06498 Human sen
34	282	29.3	113	2	AAV06505 Human sen
35	282	29.3	113	2	AAV06504 Human sen
36	274	28.5	113	2	AAV06497 Human sen
37	272	28.3	113	2	AAV06507 Human sen
38	272	28.3	113	2	AAV06507 Human sen
39	235	24.4	97	2	AAV06494 Human sen
40	235	24.4	97	3	ABD43284 Human ORF
41	238	23.7	43	4	ABG22655 Novel hum
42	218	23.7	43	4	ABG22656 Novel hum
43	214.5	22.3	124	4	ABU16331 Human nov
44	214.5	22.3	124	6	ABU55400 Human nov
45	213	22.1	88	3	AAE58912 Breast an

ALIGNMENTS

RESULT 1	AAB19160 standard; protein; 108 AA.
AC	AAAB19160;
DT	19-FEB-2001 (first entry)
XX	
DE	Amino acid sequence of human ring finger protein ROC1.
XX	
KM	ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;
KW	cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
KW	tumour.
XX	
OS	Homo sapiens.
XX	
PN	WO200058472-A2.
PD	05-OCT-2000.
XX	
PF	31-MAR-2000; 2000MO-US008592.
XX	
PR	31-MAR-1999; 99US-0127261P.
PR	22-NOV-1999; 99US-0166927P.
PA	(UYNC-) UNIV NORTH CAROLINA.
PI	Xiong Y, Ohta T;
XX	
DR	WPI; 2000-647235/62.
XX	
PT	N-PSDB; AAA68882.
PT	Novel nucleic acid encoding cullin regulating ring finger proteins,
PT	termed as ROC proteins similar to anaphase-promoting complex 11, for

Thu Mar 25 10:42:33 2004

us-09-914-324a-3.rag

Page 2

therapeutic and diagnostic use.

Claim 9; Fig 2A; 83pp; English.

The present sequence represents a human ROC1 ring finger protein. The specification also describes human ROC2, ROC1 and ROC2 are similar to Apcl1, a subunit of the APC complex. The proteins stimulate cullin essential ubiquitin ligase activity. ROC1 functions in vivo as an essential regulator of CDK inhibitor Sic1 degradation by the SCF (undefined) pathway. ROC proteins are useful for screening bioactive agents that interfere with the binding of ROC proteins with cullin proteins. Pharmaceutical formulations comprising ROC proteins are useful for diagnostic and therapeutic purposes, preferably for diagnosing and treating tumours

Sequence 108 AA;

Alignment Scores:

Pred. No.:	3,43e-57	Length:	108
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	64.03%	Indels:	0
DB:	3	Gaps:	0

US-09-914-324A-3 (1-508) x AAB19160 (1-108)

QY 7 ATGCGCGAGCGATGATGTGATACCCGAGCGACCAACAGCGCGCGGCAAGAG 66

Db 1 MetAlaIaIaMetAlaPValaAspThrProSerGlyThaAsnSerGlyAlaGlyLeuLys 20

QY 67 CGCTTTAAATGAAAAAGATGATGACATGAGCCCTCGGCGCTCGAGATATTGCGTTGAT 128

Db 21 ArghegInuValLysuStrPaenAlaValAlaLeuTriPalatTPaPILeValValaAsp 40

QY 127 AACTGTCGCATCTGCGAGGAGACCACTTATGATGATTTGATGATGACGATTAACAG 168

Db 41 AsnGysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60

QY 187 GCGTCGCTACTTTCAGAAAGATGTACTGTTCGACATGCGGAGAGTGTGTAAACATGCTTTTCAC 248

Db 61 AlasezAlaThrSerGluGluGlnCysThrValAlaIleTPGlyValCysAsnHisAlaIlePheHis 80

QY 247 TTCACATGCATTCCTCGCTGCGTCGTCGCAAAACAGACAGGAGTGTCATTTGACACAGAGAG 306

Db 81 PheHisCysIleSerAlaGlyTrpLeuLysuStrHArgGlnValCysProLeuAspAsnArgGlu 100

QY 307 TGGGATATTCGAAAAGCTATGGGCAC 330

Db 101 TrpGluPheGlnLysuTyrgLysHis 108

RESULT 2

AAB08813 ID AAB08813 standard; protein; 108 AA.

XX AAB08813;

XX 02-JAN-2001 (first entry)

XX A human cullin-interacting RING-H2 finger protein (Rbx1).

XX Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;

XX tumour suppressor; carcinoma; Ring box associated carcinoma;

XX von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;

XX cerebellar hemangioblastoma; hemangioma; retinal angliomata;

XX pheochromocytomas.

XX Homo sapiens.

XX WO200050445-A1.

XX 31-AUG-2000.

Pf		25-FEB-2000; 2000MOW-USO04838.
Pr		26-FEB-1999; 99US-0121787P.
Px	(OKLA-) OKLAHOMA MEDICAL RES FOUND.	
Rn		
Sr	Conaway JA, Conaway RC, Kamura T,	
Dc	WPI, 2000-572067/53.	
N-PDSB;	AAA7497g.	
Ct	Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and SKP1-Cdc53p-F-box protein (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box protein associated carcinomas.	
Ft		
Bt	Claim 1, Page 34, 37pp; English.	
Jl		
Xm	The present sequence represents a human cullin-interacting RING-H2 finger protein (Ring box protein), designated Rpbl. The polypeptide is a tumour suppressor. Rpbl is useful for diagnosing a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting metabolically deficient system in animals. Rpbl is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Rpbl can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau) complex controlling the conjugation of ubiquitin or ubiquitin-like proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cerebellar hemangioblastomas and hemangiomata, retinal angiomatosa and pheochromocytomas	
Cc		
Gc		
Tc		
Oo	Sequence 108 AA:	
Aa		
Alignment Scores:		
Pred. No.: 3.43e-67 Length: 108		
Percent Similarity: 616.00 Matches: 108		
Score: 100.00% Conservative: 0		
Best Local Similarity: 100.00% Mismatches: 0		
Query Match: 64.03% Indels: 0		
DB: 3 Gaps: 0		
US-09-914-324A-3 (1-508) X AAB08813 (1-108)		
QY	7 ATGGCGGACCCGTAGTATGCATTGCCGACCACCAACAGCGCGGGAAGAAG	66
Db	1 MetAlalalaIetacspValasphmrProserelynrhasnsedLyaaaglyVvylvs	20
OY	67 CGCTTTAAACTGMAAAAAAGTGTAATCAGTAGCCCTCTGGSCCTGGGATATTTGGTTGAT	128
Db	21 ArtpheglvalyalsysrtprasnlaIavallaleutrpalatraspllevalvalasp	40
OY	127 AACGTGGCATCTGCAGAACACAATTATGTGATCTTTGCATAGATGTCAAAGTCATAACAG	188
Db	41 AmcyAlalaiIecysargshmsrlIethcaspleucysileglnucygainlasmgIn	60
OY	187 GCCTCGGCTACTTCAANAAGAGTGKCTGTGGCANRGGSGAGTCTGTAAACATGCTTTTCAC	246
'Db	61 AlaserlalhsertclugduysrhvalaalrrpglyvalCyssasmhlslalaphehis	80
OY	247 TTCACATGCATCTCTGGCTGAGCTCAAAACAGCACAGAGTGTTCATTGTGACACAGAG	306
Db	81 PhehiICysilleserxtgrtlepuhystrhxrglnvalCsproLeuaAspmarsgIn	100
OY	307 TTGGAAATTCCAAAAGATGAGGAC	330
Db	101 TrpdluPhedinlysfriclyHis	108
RESULT 3		
AAFG03890		
ID	AAF03890 standard; protein; 108 AA.	
XX		
AC	AAF03890;	

[illegible][illegible]

QY	247	TTCCACGCGACATCTCTCCCTGGCTCAAAACACGACAGGTGTGTCATTGGACACAGAG	300
Db	81	PheHisCysHisSerArgIleTyrPheLeuTyrThrArgIleValCysProLeuAspAsnArgGlu	100
QY	307	TGGGATATTCCAAAGTATGGGCAC	330
Db	101	TrpIuPheGlnLysTyrGlyHis	108
RESULT 4			
ID	AAA47599	standard; protein; 108 AA.	
XX	AAA47599;		
XX	07-JAN-2002	(first entry)	
XX	ROCI.		
XX	Assay: ubiquitin ligase; tag1-ubiquitin; E1; E2;		
XX	ubiquitin activating enzyme; ubiquitin conjugating enzyme; E3;		
XX	ubiquitin ligase; ubiquitination modulator.		
XX	Unidentified.		
XX	WO200175145-A2.		
XX	11-OCT-2001.		
XX	03-APR-2001; 2001WO-US010906.		
XX	03-APR-2000; 2000US-00542497.		
XX	(RIGE-) RIGEL PHARM INC.		
XX	Issakani SD, Huang J, Sheung J, Pray TR;		
XX	WPI; 2001-626445/72.		
XX	Assaying ubiquitin ligase activity for identifying modulators of		
XX	ubiquitination. By combining ubiquitin, ubiquitin activating conjugating		
XX	enzyme, ubiquitin ligase and measuring amount of ubiquitin bound to the		
XX	ligase.		
XX	Example 1; Fig 11; 98pp; English.		
XX	The sequences given in AAA47596-602 are proteins which may be used in the		
XX	method of the invention for assaying ubiquitin ligase activity. The		
XX	method comprises combining under conditions that favour ubiquitin ligase		
XX	activity, tag1-ubiquitin, E1 (ubiquitin activating enzyme), E2 (ubiquitin		
XX	conjugating enzyme) and E3 (ubiquitin ligase) and measuring the amount of		
XX	tag1-ubiquitin bound to the E3. The method is useful for assaying which		
XX	ubiquitin ligase activity and ubiquitination enzyme activity which is		
XX	useful for identifying ubiquitination modulator. The method comprises		
XX	combining tag1-ubiquitin, the modulator, E1, E2 and tag2-E3 and measuring		
XX	the amount of tag1-ubiquitin bound to tag2-E3 or combining tag1-		
XX	ubiquitin, modulator, E1 and tag3-E2 and measuring the amount of tag1-		
XX	ubiquitin bound to tag3-E2. Ubiquitin ligase activity is measured		
XX	directly, eliminating the need for target proteins and subsequent		
XX	analysis such as separating ligated from unligated material in an SDS-		
XX	PAGE procedure. This allows multi-well array analysis and high throughput		
XX	screening techniques for modulators of ubiquitination activity. The		
XX	method also allows the analysis of many different combinations of E3		
XX	components and E2/E3 combinations without requiring prior identification		
XX	of specific target substrates. Ubiquitin is labeled, directly or		
XX	indirectly and this allows for easy and rapid detection and measurement		
XX	of ligated ubiquitin		
XX	Sequence 108 AA:		
Alignment Scores:			
Pred. No.:	3,43e-67	Length:	108
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00%
 Query Match: 64.03%
 DB: 4
 Gaps: 0
 Mismatches: 0
 Indels: 0

US-09-914-324a-3 (1-508) x AAE24620 (1-108)

QY 7 ATGGCGGCGAGATGATGTGATATCCCGAGCGGACCAACAGCGCGCGGCGAGAG 66
 Db 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyValys 20
 QY 67 CGCTTTGAAGTGAAGAAAAGTGAATGCGAGTACCCCTCGGGGCTGGATTTGGTTGAT 126
 Db 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 QY 127 AACTGTGCCATCTGCAGGAGACCAATTAATGATCTTTGATGATGATGATGATGATGAT 186
 Db 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 QY 187 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCGATGGGAGTGTGATGATGATGATGATGAT 246
 Db 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis 80
 QY 247 TTCACATGATCTCTCGCTGGCTCAAAACAGACAGAGTGTGTCCATTGAGACACAGAGAG 306
 Db 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 QY 307 TGGGAATTCCAAAGTATGGGCAC 330
 Db 101 TrpGluPheGlnLysTrpGlyHis 108

RESULT 5

AAE24620
 ID AAE24620 standard; protein; 108 AA.

AAE24620;

22-OCT-2002 (first entry)

Human RING finger protein, ROC1.

Ubiquitin ligase; Ub; tag1-ubiquitin; E1; ubiquitin-activating enzyme;

E2; ubiquitin-conjugating enzyme/ubiquitin carrier protein; E3; human;

RING finger protein.

Homo sapiens.

US2002042083-A1.

11-APR-2002.

03-APR-2001; 2001US-00826312.

03-APR-2000; 2000US-00542497.

(RIGF-) RIGEL PHARM INC.

Issakani SD, Huang J, Sheung J, Pray TR;

WPI; 2002-488718/52.

Assay for ubiquitin ligase activity, useful for identifying modulators,

by measuring binding of labeled ubiquitin to ubiquitin ligase.

Disclosure; Fig 11; 56pp; English.

The invention relates to an assay for ubiquitin ligase (UL) activity

which comprises incubating tag1-ubiquitin, E1 (ubiquitin-activating

enzyme), E2 (ubiquitin-conjugating enzyme/ubiquitin carrier protein) and

E3 (UL) and measuring the amount of tag1-ubiquitin bound to E3. The

method is particularly used to screen for modulators of UL activity. The

present sequence is human RING finger protein, ROC1

Sequence 108 AA;

Alignment Scores:
 Pred. No.: 3,43e-67
 Score: 616.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 64.03%
 DB: 5
 Gaps: 0
 Length: 108
 Matches: 108
 Conservative: 0
 Mismatches: 0
 Indels: 0

US-09-914-324a-3 (1-508) x AAE24620 (1-108)

QY 7 ATGGCGGCGAGATGATGTGATATCCCGAGCGGACCAACAGCGCGCGGCGAGAG 66
 Db 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyValys 20
 QY 67 CGCTTTGAAGTGAAGAAAAGTGAATGCGAGTACCCCTCGGGGCTGGATTTGGTTGAT 126
 Db 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 QY 127 AACTGTGCCATCTGCAGGAGACCAATTAATGATCTTTGATGATGATGATGATGATGAT 186
 Db 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 QY 187 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCGATGGGAGTGTGATGATGATGATGATGAT 246
 Db 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis 80
 QY 247 TTCACATGATCTCTCGCTGGCTCAAAACAGACAGAGTGTGTCCATTGAGACACAGAGAG 306
 Db 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 QY 307 TGGGAATTCCAAAGTATGGGCAC 330
 Db 101 TrpGluPheGlnLysTrpGlyHis 108

RESULT 6

ADC02481
 ID ADC02481 standard; protein; 108 AA.

ADC02481;

18-DEC-2003 (first entry)

RING finger protein ROC1.

ubiquitin; Mdm2; p53; RING finger protein; ROC1.

Unidentified.

US2003104474-A1.

05-JUN-2003.

26-MAR-2002; 2002US-00108767.

03-APR-2000; 2000US-00542487.

03-APR-2001; 2001US-00826312.

04-MAR-2002; 2002US-00091139.

(ISSA/) ISSAKANI S D.

(HUAN/) HUANG J.

(SHEU/) SHEUNG J.

(PRAY/) PRAY T R.

Issakani SD, Huang J, Sheung J, Pray TR;

WPI; 2003-787056/74.

Assaying for candidate agent that modulates attachment of ubiquitin

moieties to Mdm2 protein comprises combining ubiquitin agent comprising

ubiquitin moiety, Mdm2 protein, and candidate agent.

Disclosure; Fig 11; 96pp; English.

XX	The present sequence represents a method of assaying for a candidate
CC	agent that modulates the attachment of a ubiquitin moiety to an Mdm2
CC	protein. The method is useful for assaying for a candidate agent that
CC	modulates the attachment of a ubiquitin moiety to an Mdm2 or p53 protein.
CC	The present sequence represents the amino acid sequence of RING finger
CC	protein ROC1.
XX	
SO	Sequence 108 AA:
Alignment Scores:	
Pred. No.:	3,43e-67
Score:	616.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	64.03%
DB:	7
Gaps:	0
US-09-914-324A-3 (1-508) X ADC02481 (1-108)	
QY	7 ATGGCGGACGATGATGTGTGATATCCCGAGCGCACCAACAGGGCGCGGACAGAG 66
DB	1 MetAlaIaIaIaMetAspValaSpTRProSerGlyThrAsnSerGlyAlaGlyLys 20
QY	67 CGCTTTAAATGAAAAGATGGAATGAGATGAGCCCTCTGGGCTGGGATATTGTGGTGA 126
DB	21 ArgPheIuValIysLysITTPheAlaIaValaIaLeuITTPAlaITPAspIleValaVala 40
QY	127 AACTGTCCATCTGCAGGAACCAATTAATGATCTTTGCATPAGAAATGTCAAGCTAAC 186
DB	41 AsnLysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
QY	187 GCGGCGGCTCTTCAGAGAAGTGTACTGTGGATGGAGGAGTGTGTAAACATGCTTTTCAC 246
DB	61 AlaSerAlaThrSerGluGluGlySerThrValaIaITPGLyValCysAsnHLeAlaPheHis 80
QY	247 TTCATGCTGATCTCTCGCTGCTCAAAACAGACAGAGTGTGTCATTGGACACAGAG 306
DB	81 PheIleCysIleSerArgITPLeuLysITPArgIuValaCysProLeuAspAsnArgGlu 100
QY	307 TGGGAATTCCAAAGATGAGGCAC 330
DB	101 TrpIuPheGlnLysITryGlyHis 108
RESULT 7	
ID	ABB68080 standard; protein; 108 AA.
XX	ABB68080;
AC	
XX	26-MAR-2002 (first entry)
DT	
XX	Drosophila melanogaster poly(amide) SQ ID NO 31032.
DE	
XX	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US009231.
XX	
PR	23-MAR-2000; 2000US-0191637P.
XX	
PR	11-JUL-2000; 2000US-00614150.
XX	
PA	(PEKE) PE CORP NY.
XX	
PI	Venter JC, Adams M, Li FMD, Myers EW;
XX	
DR	WPI; 2001-656860/75.

DR	N-PSDB; ABLI2183.
XX	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	genes from Drosophila and for elucidating cell signaling and cell-cell
PT	interactions.
XX	
PS	Disclosure; SEQ ID NO 31032; 21bp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The invention is
CC	useful in developmental biology and in elucidating cell signalling and
CC	cell-cell interactions in higher eukaryotes for the development of
CC	insecticides, therapeutics and pharmaceutical drugs. The invention
CC	discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA
CC	sequences (ABLI01840-ABLI6175) and the encoded proteins (ABBS7737-
CC	ABBS72072). The sequence data for this patent did not form part of the
CC	printed specification, but was obtained in electronic format directly
CC	from WIFO at ftp.wifo.int/pub/published_pct_sequences
XX	
SQ	Sequence 108 AA:
	Alignment Scores:
	Pred. No.: 5,22e-57 Length: 108
	Score: 534.00 Matches: 95
	Percent Similarity: 90.83% Conservative: 4
	Best Local Similarity: 87.16% Mismatches: 4
	Query Match: 55.51% Indels: 6
	DB: Gaps: 2
US-09-914-324A-3 (1-508) x ABB69080 (1-108)	*
OY	ATGAGATGTGGAT-----ACCCGAGCGGCACCAACAGCGCGCGGCGAG 63
Dd	1 MetcIvalAspIunApGIyTyrGluaIProSerSerSerSerlyGly---AspLys 19
OY	AAGCGCTTTGAATGAAAGAAGTGGAATGAGAGCCCTGGGCGTGGATATTGGTT 122
Dd	20 LysrGrHeGluValIylsLyStrpsnAlaValAlaLeutrpAlatrpAspIlleVal 39
OY	GATAACAGTGCATCTGCAGAACACCATTAATGATCTTTCATAGAAATGTCAAGCTAAC 183
Dd	40 AspSnnCySaIIalIecYsaTrgsnHsrIleVeaCpLeuCYsIIeGluCYGlnAlaasn 59
OY	CAGGCGTCCGCTACTTCAGAAAGCTGACTGCCATGGGAGCTGTGAACAGCTTTT 243
Dd	60 GlmlaserXlaThrSerGluGluCysHrrVaIAlatrpGlyValCYasnhIsAlaPhe 79
OY	CACATTCACATGCATCTCTCGCTGCCTCAAAAACAGCACAGGTGTGTCATTGGACAACGA 303
Dd	80 HispethisCYsIIeSerArgTrpLeuSthrAAGlnValCYspIoleuAspAsnArg 99
OY	GAGTGGGAATTCAAAAAGTAGTGGGCAC 330
Dd	100 GlutrpsApSpHeGlnIlyStrgIyHis 108
RESULT 8	
ID	AAG23004 standard; protein; 118 AA.
XX	
'AC	AAG23004;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 26148.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	

Thu Mar 25 10:42:33 2004

us-09-914-324a-3.rag

PD 06-SEP-2000.
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25-FEB-1999; 99US-0121825P.
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Alignment Scores:

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Percent Similarity: 83.76%
Best Local Similarity: 78.63%
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Gaps: 2
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US-09-914-324a-3 (1-508) x AAG23004 (1-118)

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Db 102 GluValCySerIleuAspSensergIuTrpGluPheGlnIuLysTrpGlyHis 118
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XX
AC AAG23005;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 26149.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
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 AC ABB66109;
 XX 26-MAR-2002 (first entry)
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 25119.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 KM Drosophila melanogaster.
 OS Drosophila melanogaster.
 XX WO200171042-A2.
 FN 27-SEP-2001.
 XX 27-SEP-2001.
 PF 23-MAR-2001; 2001WC-US009231.
 XX 23-MAR-2001; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) FE CORP NY.
 PA Venter JC, Adams M, Li FWD, Myers EM.
 PI WPI; 2001-656860/75.
 DR N-PSDB; ABL10212.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PS Disclosure; SEQ ID NO 25119; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB110511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins (AB55737-
 CC AB872072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcr_sequences
 XX Sequence 122 AA;
 SQ
 Alignment Scores:
 Pred. No.: 2.07e-40 Length: 122
 Score: 400.50 Matches: 70
 Percent Similarity: 77.57% Conservative: 13
 Best Local Similarity: 65.42% Mismatches: 19
 Query Match: 41.63% Indels: 5
 DB: 4 Gaps: 2
 US-09-914-324A-3 (1-508) X ABB66109 (1-122)

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 QY 187 GCGTCCGCTACTTCAAGAAAGTGTACTGTGCGATGGAGTGTGCAATGCAACAGCTTTAC 246
 Db 75 ProAsnAlaAsnGlnMetGluCysThrValAlaTrpGlyGluCysAsnHisAlaPheHis 94
 QY 247 TTCACATGCATCTCTGCTGCTGCTCAAAACACGACGAGTGTGCTCATGGACACAGAG 306
 Db 95 TyrHisCysIleLeuAlaArgTrpLeuValArgLeuValCysProLeuAspAsnGlu 114
 QY 307 TGGGAATTCGAAAGATAGG 327
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 ID AAB08814 standard; protein; 121 AA.
 AC AAB08814;
 XX 02-JAN-2001 (first entry)
 DT 02-JAN-2001 (first entry)
 DE A yeast cullin-interacting RING-H2 finger protein (Rbx1).
 XX Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
 KM tumor suppressor; carcinoma; Ring box associated carcinoma;
 KM von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
 KM cerebellar hemangioblastoma; hemangioma; retinal angioma; pheochromocytomas.
 KM Saccharomyces cerevisiae.
 OS Saccharomyces cerevisiae.
 XX WO200050445-A1.
 FN 31-AUG-2000.
 XX 31-AUG-2000.
 PD 25-FEB-2000; 2000WC-US004838.
 XX 25-FEB-2000; 2000WC-US004838.
 PF 26-FEB-1999; 99US-0121787P.
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA Conway JA, Conway RC, Kamura T;
 PI Conway JA, Conway RC, Kamura T;
 DR WPI; 2000-572067/53.
 DR N-PSDB; AAA74979.
 XX Cullin interacting RING-H2 finger protein, a component of von Hippel-
 PT Lindau tumor suppressor complex and Shp1-Cdc53p-F-box protein (SCF)
 PT ubiquitin ligase, useful for diagnosing and treating Ring box protein
 PT associated carcinomas.
 PS Disclosure; Page 34-35; 37pp; English.
 XX The present sequence represents a yeast cullin-interacting RING-H2 finger
 CC protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide
 CC is a tumor suppressor. Human Rbx1 is useful for diagnosing a
 CC predisposition of a patient to certain carcinomas. It is also useful for
 CC treating Ring box protein associated carcinomas or augmenting
 CC metabolically deficient system in animals. Human Rbx1 is also useful for
 CC evaluating the effectiveness of a therapeutic treatment for Ring box
 CC associated carcinomas. Human Rbx1 can be used to screen for agents which

DE	Human novel secreted protein, Seq ID 826.
XX	
XX	Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KM	cardiac; vasotropic; cerebroprotective; neurotropic; neuroprotection;
KM	antibacterial; virucide; fungicide; optalmalogical; vulnerary;
KM	secreted protein; Rheumatoid arthritis; hyperproliferative disorder;
KM	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KM	cerebral ischaemia; angiogenesis; nervous system disorder;
KM	Alzheimer's disease; infection; ocular disorder; corneal infection;
KM	wound healing; epithelial cell proliferation; skin aging; food additive
XX	preservative; antiproliferative.
OS	Homo sapiens.
XX	
PN	WC020155322-A2.
PD	
XX	02- <i>AUG</i> -2001.
XX	
PE	17-JAN-2001; 2001MO-US001341.
XX	
PR	31-JUN-2000; 2000US-0179065P.
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PR	02-MAR-2000; 2000US-0186350P.
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PR	08-SEP-2000; 2000US-0232060P.
PR	08-SEP-2000; 2000US-0232081P.
PR	12-SEP-2000; 2000US-0231968P.

CC This sequence represents a novel human redox-sensitive, haem-binding
CC protein with a zinc RING finger domain that is encoded by the SAG gene
CC (see AX87114). SAG promotes cell growth, protects cells from apoptosis,
CC scavenges oxygen radicals and can be used for the reversion of a tumour
CC phenotype. SAG is highly conserved among species. Disruption in yeast was
CC shown to be lethal. SAG deletion mutants (see AX87315-16) have been
CC identified in human cancer lines, suggesting a role in carcinogenesis.
CC SAG genes, and mutant SAG genes, can be used to protect cells from
CC apoptosis induced by redox reagents. Antisense SAG genes can be used to
CC inhibit the growth of tumour cells. The SAG genes can also be used for
CC the recombinant production of the SAG proteins. The SAG proteins can be
CC used to scavenge oxygen radicals in organisms and to promote wound
CC healing. They are also ideal molecular targets in the development of
CC drugs against neurodegenerative disorders, cancers and muscle dystrophy
XX

SQ Sequence 113 AA

Alignment Scores:

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Best Local Similarity:	50.52%	Mismatches:	30
Query Match:	30.35%	Indels:	4
DB:	2	Gaps:	2

US-09-914-324a-3 (1-508) x AY06492 (1-113)

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QY 37 AGCGGACCAACGCGCGCGCAAGCGCTTTGAAGTGAATAAAGTGAATGCACTA 96
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 20 SerGlySerLysSerGly---GlyAspLysMetPheSerLeuLysLysTrpAsnIaVal 38
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 97 GCCCTCTGGGCGCTGGATATTGTTGATTAACTGTGCCATCTGCAGAACCACTATG 156
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 AlMetTrpSerTrpAspValGluCysAspTrnCysAlaIleCysArgValGlnValMet 58
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 157 GATCTTTGCATAGATGTCAGCTAACCGCGCTCCGCTACTTCAAGAAAGTGTACTGTC 216
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 59 AspAlaCysLeuArgCysGlnIaGluAsn-----LysGlnGlnAspCysValVal 75
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 GCATGGGAGTCTGTGAACCATGCTTTTCACTTCCACTGCATGCTCTGCTGCTCAAAACA 276
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 76 ValTrpGluCysAsnHisSerPheHisAsnCysCysMetSerLeuTrpValLysGln 95
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 CGACAGGTGTGTCATTGACAAACAGAGAGTGGGAATCCAAAGTATGGG 327
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 96 AsnAsnArgCysProLeuCysGlnGlnAspTrpValValGlnArgIleGly 112
    |||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: March 25, 2004, 09:21:17
Job time : 55.5 secs


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QY 67 CGCTTGAAGTGAAGTGAATGAGTACGCTCTGGCGCTGGGATATTGGTTGAT 126
Db 2 LysValIylsIleCysStrpAsnGlyValAlaThrIleuTriPValAlaAsnAspGlu 21
QY 127 AACTGGCCATCTGCAGGAACACATTATGATCTTGCATAGATGCAAGTCAACAG 186
Db 22 AsnCySgIlyIleCysArgMetAlaPheAsnGlyCysCysProAspCysIlys----- 38
QY 187 GCGTCCGCTACTTCCAGAAAGTGTACTGCTCCAGTGGGAGTCTGTACCATGCTTTTCA 246
Db 39 -----ValProGlyAspAspCysProLeuValIlePrgIlyGlnCysSerHisCysPheHis 56
QY 247 TTCGACTGATCTCTGCTGGCTCAAACACAGAGGTG-----TGTCCATTGGAC 297
Db 57 MethCysIleLeuIlyStrpLeuHisAlaGlnGlnValGlnGlnHisCysPrometCys 76
QY 298 AACAGAGAGTGGGAATTCGAAAG 321
Db 77 ArgGlnGluTriPlysPheIysGlu 84

RESULT 2
US-09-621-976-5805
; Sequence 5805, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO: 5805
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -109...-1
US-09-621-976-5805

Alignment Scores:
Pred. No.: 2,69e-15 Length: 112
Score: 194.50 Matches: 39
Percent Similarity: 54.29% Conservative: 18
Best Local Similarity: 37.14% Mismatches: 32
Query Match: 20.22% Indels: 16
DB: 4 Gaps: 4

US-09-914-324a-3 (1-508) x US-09-621-976-5805 (1-112)
QY 67 CGCTTGAAGTGAAGTGAATGAGTACGCTCTGGCGCTGGGATATTGGTTGAT 126
Db 2 LysValIylsIleCysStrpAsnGlyValAlaThrIleuTriPValAlaAsnAspGlu 21
QY 127 AACTGGCCATCTGCAGGAACACATTATGATCTTGCATAGATGCAAGTCAACAG 186
Db 22 AsnCySgIlyIleCysArgMetAlaPheAsnGlyCysCysProAspCysIlys----- 38
QY 187 GCGTCCGCTACTTCCAGAAAGTGTACTGCTCCAGTGGGAGTCTGTACCATGCTTTTCA 246
Db 39 -----ValProGlyAspAspCysProLeuValIlePrgIlyGlnCysSerHisCysPheHis 56
QY 247 TTCGACTGATCTCTGCTGGCTCAAACACAGAGGTG-----TGTCCATTGGAC 297
Db 57 MethCysIleLeuIlyStrpLeuHisAlaGlnGlnValGlnGlnHisCysPrometCys 76
QY 298 AACAGAGAGTGGGAATTCGAAAGT-----ATGGCACTAGG-----AA 336
Db 76 sarGlnAsnGlySerSerArgSerGlnAlaArgProGlySerArgIlePrgIlyLeu 96
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QY 337 AAGACTCTTCCA 349
Db 96 uArgLeuLeuPrg 100

RESULT 3
US-09-621-976-5677
; Sequence 5677, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO: 5677
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -106...-1
US-09-621-976-5677

Alignment Scores:
Pred. No.: 3.56e-15 Length: 112
Score: 193.50 Matches: 38
Percent Similarity: 54.63% Conservative: 21
Best Local Similarity: 35.19% Mismatches: 33
Query Match: 20.11% Indels: 16
DB: 4 Gaps: 4

US-09-914-324a-3 (1-508) x US-09-621-976-5677 (1-112)
QY 67 CGCTTGAAGTGAAGTGAATGAGTACGCTCTGGCGCTGGGATATTGGTTGAT 126
Db 2 LysValIylsIleCysStrpAsnGlyValAlaThrIleuTriPValAlaAsnAspGlu 21
QY 127 AACTGGCCATCTGCAGGAACACATTATGATCTTGCATAGATGCAAGTCAACAG 186
Db 22 AsnCySgIlyIleCysArgMetAlaPheAsnGlyCysCysProAspCysIlys----- 38
QY 187 GCGTCCGCTACTTCCAGAAAGTGTACTGCTCCAGTGGGAGTCTGTACCATGCTTTTCA 246
Db 39 -----ValProGlyAspAspCysProLeuValIlePrgIlyGlnCysSerHisCysPheHis 56
QY 247 TTCGACTGATCTCTGCTGGCTCAAACACAGAGGTG-----TGTCCATTGGAC 297
Db 57 MethCysIleLeuIlyStrpLeuHisAlaGlnGlnValGlnGlnHisCysPrometCys 76
QY 298 AACAGAGAGTGGGAATTCGAAAGT-----ATGGCACTAGGAAAAAGTTTTC 348
Db 76 sarGlnAsnGlySerSerArgSerGlnAlaArgProGlySerArgIlePrgIly 93
QY 349 ATCAAGCTTAATGTTTGTTA 370
Db 94 -----GlyIleLeuIleLeuLeu 99

RESULT 4
US-09-621-976-5714
; Sequence 5714, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
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NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5714
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -53..-1
NAME/KEY: UNSURE
LOCATION: 14
OTHER INFORMATION: Xaa = Glu,Gln
US-09-621-976-5714

Alignment Scores:
Pred. No.: 0.000198
Score: 105.50
Percent Similarity: 56.10%
Best Local Similarity: 36.59%
Query Match: 10.97%
DB: 4
Gaps: 1

US-09-914-324A-3 (1-508) x US-09-621-976-5714 (1-94)

QY 148 CACATTATGATCTTTCATAGATGTCAGCTAACAGGCGCCGCTACTTCAGAGAG 207
DB 10 HistHthrspAlaAlaProAspCysAla-----ValProGlyAspAsp 24

QY 208 TGTAATGTCGATGGAGGATGTCGTAACCATGCTTTTCATCTGCATGTCATCTGCGCTGG 267
DB 25 CysProLeuValTrpGlyGlnCysSerHisCysPheHisMetHisCysIleLeuLysTrp 44

QY 268 CTC 270
DB 45 Leu 45

RESULT 5
US-09-325-932A-49
Sequence 49, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Film, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325, 932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 49
LENGTH: 104
TYPE: PRT
ORGANISM: Pinus radiata
US-09-325-932A-49

Alignment Scores:
Pred. No.: 0.0665
Score: 85.00
Percent Similarity: 39.47%
Best Local Similarity: 26.32%
Query Match: 8.84%
DB: 4
Gaps: 1

US-09-914-324A-3 (1-508) x US-09-325-932A-49 (1-104)

QY 130 TGTGCATCTGCAGAGACCATATGATCTTTCATAGATGTCAGCTAACAGGCG 189
DB 25 CysAlaValCysLeuSerLysPheGluAspIle----- 35

QY 190 TCCGCTACTCAGAGAGATGATGTCATGCGATGGGAGTCTGTAAACCATGCTTTTCATCTC 249
DB 36 -----GluIleLeuArgPheLeuProLysCysArgHisAlaPheHisIle 50

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QY 250 CACTGCATCTCTCGCTGCTCAAAAACAGCAGGATGTGTCCATTGACACAGAGATGC 309
DB 51 AspCysIleAspTrpTrpLeuGlnLysHisSerSerCysProLeuCysArgHisLysVal 70

QY 310 GAATTCCAAAGTATGGGCACTAGAGAAAAGACTTCTTCGCATCAAGCTT 357
DB 71 SerAlaGluAspProAlaAsnPheThrTrpThrAsnSerMetArgLeu 86

RESULT 6
US-09-268-140-2
Sequence 2, Application US/09268140
Patent No. 6268176
GENERAL INFORMATION:
APPLICANT: Gemmill, Robert M.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
FILE REFERENCE: 93445-00004
CURRENT APPLICATION NUMBER: US/09/268, 140
CURRENT FILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: US 60/077,723
PRIOR FILING DATE: 1998-03-12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 664
TYPE: PRT
ORGANISM: Homo sapiens
US-09-268-140-2

Alignment Scores:
Pred. No.: 0.129
Score: 85.00
Percent Similarity: 40.48%
Best Local Similarity: 28.57%
Query Match: 8.84%
DB: 3
Gaps: 4

US-09-914-324A-3 (1-508) x US-09-268-140-2 (1-664)

QY 64 AAGCGCTTGAAGTAAAGTGAATGCAGAGCCCTGTGGCGCTGGATATT----- 117
DB 522 ArgArgThrAlaValLysLysLysLeuSerLeuPro-----GluIleLysGly 537

QY 118 -----GTGGTATATGCTGTGCATCTGCAGAGACCATTAATGATCTT 162
DB 538 SerArgLeuGlnGluLysAlaAspValCysAlaIleCysTyrHisGluPhe----- 554

QY 163 TGCATAGATGTCAGAGTCAACAGGCGCCGCTACTTACAGAGAGTACTGTCATGG 222
DB 555 -----ThrThrSerAlaArgIleThr----- 561

QY 223 GGAGTGTAAACCATGCTTTTCATCTTCACATGTCATCTGCTGGCTGCAAAACAGCAG 282
DB 562 ---ProCysAsnHisTyrPheHisAlaLeuCysIleuArgLysTrpLeuLysTrpIleGlnAsp 580

QY 283 GTGTGTCATTTG 294
DB 581 ThrCysProMet 584

RESULT 7
US-09-828-303-18
Sequence 18, Application US/09828303
Patent No. 6677504
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNETT, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, RUYTING
TITLE OF INVENTION: TRANSCRIPTION FACTOR STRESS-RELATED PROTEINS AND
FILE REFERENCE: 16313-0030
CURRENT APPLICATION NUMBER: US/09/828, 303

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/ CURRENT FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: 60/196,001
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 79
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 18
/ LENGTH: 337
/ TYPE: PR
/ ORGANISM: Physcomitrella patens
US-09-828-303-18

Alignment Scores:
Pred. No.: 0.178 Length: 337
Score: 83.00 Matches: 17
Percent Similarity: 41.38% Conservative: 7
Best Local Similarity: 29.31% Mismatches: 20
Query Match: 8.63% Indels: 14
DB: 4 Gaps: 2

US-09-914-324A-3 (1-508) x US-09-828-303-18 (1-337)

QY 121 GTTGATTAAGTGGCCATCTGACGAGAACCATATGATCTTTGCATGAAATGTCAGCT 180
DB 85 ValPheGluCysAlaValCysLeuGlu-----GluPheGluLeu 97
QY 181 AACGAGCGCTCCGCTACTTCAGAGAGTGTACTGTGCATGGGAGTGTGTACCATGCT 240
DB 98 GlyAluValGlyAlaGlyThrLeuProlys-----CysAspHisSer 110
QY 241 TTTCACTTCACATCTCTGCTGCTGCTCAAAACAGCAGAGTGTTCATTTG 294
DB 111 PheHisLeuAspCysLeuAspMetTrpLeuHisSerHisSerThrCysProLeu 128

RESULT 8
US-09-252-991A-22218
/ Sequence 22218, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfeld et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 22218
/ LENGTH: 273
/ TYPE: PR
/ ORGANISM: Pseudomonas aeruginosa
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (180)
/ OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-22218

Alignment Scores:
Pred. No.: 0.29 Length: 273
Score: 81.00 Matches: 31
Percent Similarity: 34.51% Conservative: 8
Best Local Similarity: 27.43% Mismatches: 54
Query Match: 8.79% Indels: 20
DB: 4 Gaps: 4

US-09-914-324A-3 (1-508) x US-09-252-991A-22218 (1-273)

QY 349 TGAAGAAGCTTTTCTAGTACCTTTGGAATTCGCACTCTGTGTGCA---.293
DB 13 TrpThrCysCysValProCysArgArgSerArgGlyCysSerThrArgCysSerProAsn 32

QY 292 -----ATGACACACCTGTCTGTTTGAAGCAGGAGAGATGCGTGAAGT 245
DB 33 TrpAlaThrAlaSerAlaThrProVal-----SerProArgThrSerAlaThr 48
QY 244 GAAAGCATGTTTACAGACTCCCATGCGACAGTACACTCTTCTGAAAGGAGCGCT 185
DB 49 SerArgArgAlaSerProThrProThrSerSerThr-----AlaPro 63
QY 184 GGTTAAGTACATTTATGCAAAAGATCCATATATGTTCTTCTGAGATGCGACAGTTAT 125
DB 64 AlaSerSerProArgThrTrpArgSerProCysArgProSerCysCysTrpPysProAla 83
QY 124 CAACCAATATATCCAGCCGAGAGGCTACTG-----CATTCAGT 83
DB 84 ThrProArgCysProThrProSerSerAlaValAlaTrpGlyThrAlaGlyGlySerThr 103
QY 82 TTTCACTTCAAAGCGCTTTGCGCCGCGCGCTGTGG 44
DB 104 AlaProSerArgAlaAlaSerArgSerArgArgCysTrp 116

RESULT 9
US-08-786-606-3
/ Sequence 3, Application US/08786606
/ Patent No. 5861495
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Coleman, Roger
/ APPLICANT: Goli, Surya K.
/ TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
/ TITLE OF INVENTION: PROTEINS
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/786,606
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy R
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0173 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELERX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 180 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-786-606-3

Alignment Scores:
Pred. No.: 0.331 Length: 180
Score: 80.00 Matches: 29
Percent Similarity: 39.81% Conservative: 12
Best Local Similarity: 28.16% Mismatches: 18
Query Match: 8.32% Indels: 44

Thu Mar 25 10:42:34 2004

us-09-914-324a-3.rai

Page 6

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/06/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTNOT07
CLONE: 3217567
US-09-234-613-48

Alignment Scores:
Pred. No.:      0.331      Length:      180
Score:          80.00     Matches:    29
Percent Similarity: 39.81%   Conservative: 12
Best Local Similarity: 28.16% Mismatches:   18
Query Match:     8.32%      Indels:     44
DB:              Gaps:      7

US-09-914-324A-3 (1-508) x US-09-234-613-48 (1-180)

Cy
7 ATGCGCGCAGCATGTGATGTGAT--ACCCGAGCGGCACCAC-----AGCGGC 54
||||| | ||||| | :| | | ||||| | |||
1 MetAlaIhaIaIagIugIuaIpGIyGIyPfoGIuGIyProASnaRgIUaRgIyGIy 20
Db
55 GCGGGCGAAAGAGCGCTTTGAAGTGAAGAAAAGTGGAATGCAGTCAGCCCTCGGGCTGGAT 114
||||| | ||||| | ||||| | ||||| | ||||| |
21 AlIGdly--AlaThrPhEguL----- 26
Cy
115 ATTGTGGTGTATACTGTGCCATCTGCAGAAACAATTATGATCTTTGATGAATGT 174
||||| | ||||| | ||||| | ||||| | ||||| |
27 -----CyAsnIlleCysLeuGlL--- 32
Cy
175 CAAGCTAACCAAGCGGTCCTACTTTCAGAAGACTGACTGTGCATGGGAGACTGTAAAC 234
||||| | ||||| | ||||| | ||||| | ||||| |
33 -----TrpAlaArgGLuAlaValSer-----ValCysGly 43
Cy
235 CATGCTTTTCATCTTCACATGCATCTCTCGCTGGCTGAAAAC-----CGACAGGTG 285
||||| | ||||| | ||||| | ||||| | ||||| |
44 HisIeuYrCysTrpProCysLeuHisGlnTrpLeuGluThrArgProGIuARgIuGIu 63
Db
286 TGTCCATTG 294
||||| | ||||| | ||||| | ||||| | ||||| |
64 CysProVal 66

RESULT 12
US-08-786-606-9
; Sequence 9, Application US/08786606
; Patent No. 5861495
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Yang, Janice
APPLICANT: Coleman, Roger
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

```

```

1 COUNTRY: USA
2 ZIP: 94304
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Diskette
5 COMPUTER: IBM Compatible
6 OPERATING SYSTEM: DOS
7 SOFTWARE: FastSeq for Windows Version 2.0
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/786,606
10 FILING DATE:
11 CLASSIFICATION: 514
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER:
14 FILING DATE:
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Billings, Lucy RJ
17 REGISTRATION NUMBER: 36,749
18 REFERENCE/DOCKET NUMBER: PF-0173 US
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 415-855-0555
21 TELEFAX: 415-845-4166
22
23 INFORMATION FOR SEQ ID NO: 9:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 284 amino acids
26 TYPE: amino acid
27 STRANDEDNESS: single
28 TOPOLOGY: linear
29 IMMEDIATE SOURCE:
30 LIBRARY: GenBank
31 CLONE: 157535
32
33 US-08-786-606-9
34
35 Alignment Scores:
36 Pred. No.:
37 Score: 0.39 Length: 284
38 Percent Similarity: 80.00 Matches: 24
39 Best Local Similarity: 35.11% Conservative: 9
40 Query Match: 25.53% Mismatches: 29
41 DB: 8.32% Indels: 32
42 Gaps: 3
43
44 US-09-914-324A-3 (1-508) x US-08-786-606-9 (1-284)
45
46 Oy 13 GCAGCGATGATGTGATATACCCGCGGCAACACAGCGCGGCGCAAGACGCTT 72
47 Db 104 AAlIleMeLysIlethrIthrIlyshrlly-----LysPhe 115
48 Oy 73 GAAGTGAAGAGTGAATGACAGTAGCCCTCTGGCGCTGGGATATATGGTGTGATACTGT 122
49 Db 116 SerAspGluLys-----ApLeuaspSerAspCysCys 126
50 Oy 133 GCATCTGGAGGAGACCATTTATGATCTTTGCATAGATGTCAAGCTAACAGGCGCTCC 192
51 Db 127 AAlIleLys-----IleGlu 131
52 Oy 193 GCTACTTCAGAAAGATGTACTGTGCATGCGGAGTCTGTAACTGCTTTTCACTTCAC 252
53 Db 132 AAlATyLysProThrAspThrIleargIleuProCysLysHisGluPheHisLysAsn 151
54 Oy 253 TGCATCTCTGCTGGCTCAAAACACAGACAGAGTGTCATATG 294
55 Db 152 CysIleAspProIlePheuIleGluHisIargHrCysProwmet 165
56
57 RESULT 13
58 US-09-052-089A-15
59 ; Sequence 15, Application US/09052089A
60 ; Patent No. 6346605
61 ; GENERAL INFORMATION:
62 ; APPLICANT: Lee, Soo Y.
63 ; Choi, Yongwon
64 ; TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE TNF RECEPTOR SUPER
65 ; FAMILY, AND USES THEREOF
66 ; NUMBER OF SEQUENCES: 16

```


CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,089A
FILING DATE: 31-Mar-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-052-089A-15
Alignment Scores:
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Best Local Similarity: 29.31% Mismatches: 15
Query Match: 8.21% Indels: 16
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DB 2 AspvAlCysAlaIleCysLeuAspGluTyrGluAsp----- 13
QY 184 CAGCGTCGCCCTACTTACGAAGAGTACTGTGCATGGGAGTCTGTACCATGCTTTT 243
DB 14 -----GlyAspLysLeuArgIleLeu-----ProCysSerHisAlaTyr 26
QY 244 CACTTCACATGCATCTCTCGCTGCTC---AAACAGACAGAGTGTGCATTG 294
DB 27 HisCysLysCysValAspProIleuThrLysThrLysThrCysProVal 44
RESULT 14
US-09-663-600A-106
Sequence 106, Application US/09663600A
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclet, Aymeric
APPLICANT: Bouguetel, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677

PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 106
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -34...-1
NAME/KEY: UNSURE
LOCATION: 20,64,65,130,156,282,288,289,294,296,300,302,310
OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-09-663-600A-106
Alignment Scores:
Pred. No.: 0.562 Length: 359
Score: 79.00 Matches: 17
Percent Similarity: 46.55% Conservative: 10
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Query Match: 8.21% Indels: 16
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DB: 4
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QY 244 CACTTCACATGCATCTCTCGCTGCTC---AAACAGACAGAGTGTGCATTG 294
DB 263 HisCysLysCysValAspProIleuThrLysThrLysThrCysProVal 280
RESULT 15
US-08-867-057-1
Sequence 1, Application US/08867057
Patent No. 5840535
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Prieti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW ZINC RING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,057
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy U.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0311 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-885-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SBO ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 381 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BMAROT02
 CLONE: 104119
 US-08-867-057-1

Alignment Scores:
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 Query Match: 8.21% Indels: 16
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US-09-914-324A-3 (1-508) x US-08-867-057-1 (1-381)

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DB	250	-----	-----	-----	-----	-----	-----	-----	-----	-----	262
		-----	-----	-----	-----	-----	-----	-----	-----	-----	
QY	244	CAC	TTCCACT	GCATCT	CGCTG	CGCTC	-----	AAA	ACAG	CAGAC	AGTGT
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DB	263	His	CysLys	CysVal	AspPro	TrpLeu	ThrLys	ThrLys	LysThr	CysPro	Val
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Search completed: March 25, 2004, 09:25:16
 Job time : 23 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

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Run on:      March 25, 2004, 09:23:42 ; Search time 42.5 Seconds
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Title: US-09-914-324A-3

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Total number of hits satisfying chosen parameters: 2130338

Maximum DB seq length: 20000000000

Listing first 45 summaries

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Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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1	616	64.0	108	9	US-09-826-112-6	Sequence 6, Appl
2	616	64.0	108	14	US-10-108-767-6	Sequence 6, Appl
3	616	64.0	108	14	US-10-152-156-6	Sequence 6, Appl
4	518.5	52.7	118	12	US-10-424-599-148916	Sequence 148916
5	506.5	52.7	152	12	US-10-424-599-221431	Sequence 221431
6	420.5	43.7	106	12	US-10-424-599-148915	Sequence 148915
7	313	32.5	75	12	US-10-424-599-22014	Sequence 220014
8	294	30.6	118	9	US-09-764-664-1286	Sequence 1286, App
9	292	30.4	131	9	US-09-764-664-1285	Sequence 1285, App
10	287	29.8	64	12	US-10-424-599-228320	Sequence 228320
11	287	29.8	113	9	US-09-826-112-8	Sequence 8, Appl
12	287	29.8	113	14	US-10-108-767-8	Sequence 8, Appl
13	287	29.8	113	14	US-10-152-156-8	Sequence 8, Appl
14	282	29.3	68	12	US-10-424-599-224288	Sequence 224288
15	228	22.3	40	12	US-10-424-599-264079	Sequence 264079
16	214.5	22.3	124	9	US-09-764-664-1284	Sequence 1284, Ap
17	213	22.1	88	12	US-10-756-774-2618	Sequence 2618, Ap
18	213	22.1	88	14	US-10-102-806-620	Sequence 620, Ap
19	213	22.1	91	15	US-10-264-049-12937	Sequence 12937, Ap
20	213	22.1	105	9	US-09-764-664-1274	Sequence 1274, Ap
21	208	21.6	84	12	US-10-421-625-94	Sequence 94, App
22	208	21.6	100	12	US-10-424-599-255860	Sequence 255860
23	202.5	21.0	85	15	US-10-264-049-12926	Sequence 2926, A
24	202	21.0	84	9	US-09-826-312-2	Sequence 5, Appl
25	202	21.0	84	14	US-10-108-767-5	Sequence 5, Appl
26	202	21.0	84	14	US-10-152-156-5	Sequence 5, Appl
27	186.5	19.4	121	9	US-09-764-664-839	Sequence 839, App
28	186.5	19.4	121	9	US-09-764-664-1294	Sequence 1294, Ap
29	186.5	19.4	121	9	US-09-764-664-891-4639	Sequence 14639, App
30	175.5	18.2	114	15	US-10-330-797-3003	Sequence 3003, A
31	175	18.2	73	12	US-10-424-599-235108	Sequence 235108, A
32	164	17.0	124	12	US-10-425-114-37253	Sequence 37253, A
33	138	14.3	34	12	US-10-424-599-254645	Sequence 254645, A
34	135.5	14.3	133	14	US-10-032-585-7259	Sequence 7259, A
35	102	10.6	144	12	US-10-444-599-217773	Sequence 217773, A
36	100.5	10.6	205	12	US-10-444-599-219111	Sequence 219111, A
37	98	10.2	234	12	US-10-444-599-226133	Sequence 226133, A
38	97.5	10.1	128	12	US-10-424-599-202979	Sequence 202979, A
39	97.5	10.1	194	12	US-10-444-599-192559	Sequence 192559, A
40	97.5	10.1	195	12	US-10-425-114-36967	Sequence 36967, A
41	97.5	10.1	209	12	US-10-425-114-41399	Sequence 41399, A
42	97.5	10.1	209	12	US-10-425-114-63173	Sequence 63173, A
43	86.5	10.0	345	12	US-10-425-114-71489	Sequence 71489, A
44	86.5	10.0	356	12	US-10-444-599-179820	Sequence 179820, A
45	96.5	10.0	357	12	US-10-444-599-267968	Sequence 267968, A

ALIGNMENTS

RESULT 1
US-09-826-312-6
Sequence 6, Application US/09826312
Patent No. US20020042083A1
GENERAL INFORMATION:
APPLICANT: Issakant, Saritz D.
APPLICANT: Huang, Jianing
APPLICANT: Shuang, Julie
APPLICANT: Prey, Todd R.
TITLE OF INVENTION: UBQUITIN LIGASE ASSAY
FILE REFERENCE: A-68613-T/RMS/JUD
CURRENT APPLICATION NUMBER: US/09/826.312
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR FILING DATE: 2000-04-03

SOFTWARE: PatentIn version 3.1

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: SEQ ID NO 8
:
: LENGTH: 108
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! TYPE: PRT

US-09-826-312-6

Alignment Scores:

Pred. No.: 1.63e-61 Length: 108
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.03% Indels: 0
 DB: 9 Gaps: 0

US-09-914-324A-3 (1-508) x US-09-826-312-6 (1-108)

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 QY 67 CGCTTTGAAGTGAAGAAAGTGAATGAGTACCCCTCTGGGCTGGGATTTGTGTTGAT 126
 DB 21 ArgPheGluValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
 QY 127 AACTGTCCATCTGCGAGGAAACCATTTGATGATGATGATGATGATGATGATGATGATGAT 186
 DB 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGlyIleGluCysGlnAlaAsnGln 60
 QY 187 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTGAACCATGCTTTTCA 246
 DB 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTyrGlyValCysAsnHisAlaPheHis 80
 QY 247 TTCGACTGCATCTCTGCTGGCTGCTCAACAGCAGAGTGTGCTGATGATGATGATGATGAT 306
 DB 81 PheHisCysIleSerArgLysLysLysLysLysLysLysLysLysLysLysLysLysLys 100
 QY 307 TGGGAATTCGAAAGTATGGGCGAC 330
 DB 101 TyrGluPheGlnLysTyrGlyHis 108

RESULT 2

US-10-108-767-6
 ; Sequence 6, Application US/10108767
 ; Publication No. US20030104474A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Issakant, Sarkiz D.
 ; APPLICANT: Huang, Jianing
 ; APPLICANT: Sheung, Julie
 ; APPLICANT: Pray, Todd R.
 ; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
 ; FILE REFERENCE: A-68613-5/RMS/DCF
 ; CURRENT APPLICATION NUMBER: US/10/108,767
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 09/542,497
 ; PRIOR FILING DATE: 2000-04-03
 ; PRIOR APPLICATION NUMBER: US 09/826,312
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 10/091,139
 ; PRIOR FILING DATE: 2002-03-04
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-108-767-6

Alignment Scores:

Pred. No.: 1.63e-61 Length: 108
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.03% Indels: 0
 DB: 14 Gaps: 0

US-09-914-324A-3 (1-508) x US-10-108-767-6 (1-108)

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RESULT 3

US-10-152-156-6
 ; Sequence 6, Application US/10152156
 ; Publication No. US20030108947A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Issakant, Sarkiz D.
 ; APPLICANT: Huang, Jianing
 ; APPLICANT: Sheung, Julie
 ; APPLICANT: Pray, Todd R.
 ; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGEN
 ; FILE REFERENCE: A-68613-6/RMS/DCF
 ; CURRENT APPLICATION NUMBER: US/10/152,156
 ; CURRENT FILING DATE: 2002-05-20
 ; PRIOR APPLICATION NUMBER: US 09/542,497
 ; PRIOR FILING DATE: 2000-04-03
 ; PRIOR APPLICATION NUMBER: US 09/826,312
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 10/091,174
 ; PRIOR FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: US 10/091,139
 ; PRIOR FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: US 10/109,460
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: US 10/108,767
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: US 60/291,836
 ; PRIOR FILING DATE: 2001-05-18
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-152-156-6

Alignment Scores:

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US-09-914-324A-3 (1-508) x US-10-152-156-6 (1-108)

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 QY 187 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTGAACCATGCTTTTCA 246
 DB 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTyrGlyValCysAsnHisAlaPheHis 80
 QY 247 TTCGACTGCATCTCTGCTGGCTGCTCAACAGCAGAGTGTGCTGATGATGATGATGATGAT 306
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 QY 307 TGGGAATTCGAAAGTATGGGCGAC 330
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99	1.5	1.5
100	1.5	1.5

Db 77 AspCysValValValTrpGlyGlyCysAsnHisSerPheHisAsnCysCysMetSerLeu 96

```

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 238320
LENGTH: 64
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_57228C.1 pep
US-10-424-599-238320

Alignment Scores:
Pred. No.: 6,89e-24 Length: 64
Score: 287.00 Matches: 49
Percent Similarity: 82.54% Conservative: 3
Best Local Similarity: 77.78% Mismatches: 11
Query Match: 29,83% Indels: 0
DB: 12 Gaps: 0

US-09-914-324A-3 (1-508) x US-10-424-599-238320 (1-64)
QY 139 TGCAGGACACCATTTGATGATCTTTGCATAGATGTCAAGCTAACAGGCGTCCGCTACT 19
Db 1 Cytarabinebisbenzotriptylthyminecytosineguanineadenineglycylalapro 20
199 TCAGAAAGAGTACTCTCCATAGGGAGTCTGTAAACCATGCTTTTCACTTCACCTGCATC 25
Db 21 AAGTGGTCTTCAAAACAGACAGCGGTGTCCATTCGACCAACAGAGAGTGGAAATTCCAA 31
259 TCCGCGGTGCTCAAAACAGACAGCGGTGTCCATTCGACCAACAGAGAGTGGAAATTCCAA 31
Db 41 Serargitryptalysmethionineglutaminecysteineleucineprolineasparagine 60
QY 319 AAGTATGGG 327
Db 61 Lysetylrgly 63

RESULT 11
US-09-826-312-8
Sequence 8, Application US/09826312
Patent No. US2002042083A1
GENERAL INFORMATION:
APPLICANT: Isaekani, Sarkiz D.
APPLICANT: Huang, Jianing
APPLICANT: Sheung, Julie
APPLICANT: Pray, Todd R.
TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
FILE REFERENCE: A-68613-1/RMS/JJD
CURRENT APPLICATION NUMBER: US/09/826,312
CURRENT FILING DATE: 2001-04-03
PRIORITY APPLICATION NUMBER: US 09/542,497
PRIORITY FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-312-8

Alignment Scores:
Pred. No.: 7,79e-24 Length: 113
Score: 287.00 Matches: 48
Percent Similarity: 63.92% Conservative: 14
Best Local Similarity: 49.48% Mismatches: 31
Query Match: 29,83% Indels: 4
DB: 9 Gaps: 2

US-09-914-324A-3 (1-508) x US-09-826-312-8 (1-113)
QY 37 AGGCGACCAACAGCGCGCGGCGCAAGACGCTTTGAAGTGAAGAAAGTGAATGCAGTA 96
Db 20 Serilysermethionyl--glyasparicmetphenylserleucylsertrypsinproval 38

```


Db 41 AsnCySaIleCysArgAsnHisIleWetAspLeuCySileGluCysGlnAlaAsnGln 60
QY 187 GCGTCGGCTACTTCAGAAAGTGTACTGCGATGGGAGTGTGTAACCATGCTTTTCAC 246
Db 61 AlaseRAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
QY 247 TTCACATGCATCTCTCGTGGCTCAAAACACGACAGGTGTTCATTTGACACACAGAG 306
Db 81 PheHisCysIleSerArgTrpLeuYThrArgGlnValCysProLeuAspAsnArgGln 100
QY 307 TGGGAATTCCAAAGTATGGGCAC 330
Db 101 TrpGluPheGlnIleYTrpGlyHis 108

RESULT 2

T13388
hypothetical protein T13388.11 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13388
R:Salles, C.; Valenti, P.; Darlamitsu, A.; Henderson, N.; Campbell, L.; Glover, D.
Submitted to the EMBL Data Library, May 1999
A:Description: Sequencing the discal X chromosome of Drosophila melanogaster.
A:Reference number: Z17665
A:Accession: T13388
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-136 <CAT>
A:Cross-references: EMBL:AL031581, PIDN:CAA20888.1
C:Genetics:
A:Cross-references: Flybase:FBgn020381
A:Introns: 64/1
A>Note: BG:115C2.11

Alignment Scores:
Pred. No.: 1,76e-47 Length: 136
Score: 510.00 Matches: 95
Percent Similarity: 72.26% Conservative: 4
Best Local Similarity: 69.34% Mismatches: 4
Query Match: 53.01% Indels: 34
Gaps: 2 3

US-09-914-324a-3 (1-508) x T13388 (1-136)

QY 19 ATGATGTGAT-----ACCCGAGCGGCACCAACAGCGCGCGGCAAG 63
Db 1 MetGluValAspGluAspGlyTyrGluValProSerSerSerIysGly--AspLys 19
QY 64 AAGGGCTTTGAAGGAAAG-----84
Db 20 LysArgPheGluValLysValSerGlyGlnGlnIlySerArgValIleValAsnGln 39
QY 85 -----TGGAAATGCAGTACC 99
Db 40 CysThrAspGlyAsnThrSerSerPheProLeuArgArgLysGlnTrpAsnAlaValAla 59
QY 100 CTTGCGGCTGGGATATTGGTGTGATPACTGTCGCACTGCGAGAAACCATATGAT 159
Db 60 LeuTrpAlaTrpAspIleValValAspAsnCySaIleCysArgAsnHisIleMetAsp 79
QY 160 CTTTCATAGATGTCAAGCTAACCGGCGTCCGCTACTTCAAGAGGTGCTGTGCA 219
Db 80 LeuCySileGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAla 99
QY 220 TGGGAGTCTGTAAACCATGCTTTTCATCTTCACATTCGACGATCTCCGCTGGCTCAAAACAGA 279
Db 100 TrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuYThrArg 119
QY 280 CAGGTGTGCTCATTCGACACAGAGTGTGGAATTCCAAAGTATGGGCAC 330
Db 120 GlnValCysProLeuAspAsnArgGluTrpAspPheGlnIlyTrpGlyHis 136

RESULT 3

T47341
ring-box protein-like - Arabidopsis thaliana
N:Alternate names: Protein T21C14.50
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Aug-2002
C:Accession: T47341
R:Delserny, M.; Berger, C.; Cooke, R.; Gaubier, P.; Grellet, F.; Laudie, M.; Mewes, H.W.

Submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24462
A:Accession: T47341

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115
A:Cross-references: EMBL:AL138639
A:Experimental source: cultivar Columbia; BAC clone T21C14
C:Genetics:
A:Map position: 3
A:Introns: 43/1; 60/1; 80/1; 104/1
A>Note: T21C14.50

C:Superfamily: Yeast hypothetical protein YOL133w; RING finger homology

Alignment Scores:
Pred. No.: 2.84e-46 Length: 115
Score: 499.00 Matches: 88
Percent Similarity: 86.11% Conservative: 5
Best Local Similarity: 81.48% Mismatches: 13
Query Match: 51.87% Indels: 2
Gaps: 1

US-09-914-324a-3 (1-508) x T47341 (1-115)

QY 7 ATGGCGGCGCATGATGTGATGATACCCGAGCGGCACCAACAGCGCGCGCAAG 66
Db 10 MetGlyGluSerSerSerIleSerValProSer-----SerSerIlyAsnSerLys 27
QY 67 CGCTTGAAGTGAAAGATGTGATGTCAGTACCTCTGGGCTGGATATTGGTGTGAT 126
Db 28 ArgPheGluLeuLysLysTrpSerAlaValAlaLeuTrpAlaTrpAspIleValAlaAsp 47
QY 127 AACTGTGCATCTCGGAGAACCACTTATGATTTTGCATGATGATGCAAGCTAACCG 186
Db 48 AsnCySaIleCysArgAsnHisIleWetAspLeuCySileGluCysLeuAlaAsnGln 67
QY 187 GCGTCGGCTACTTCAGAAAGTGTACTGCGATGGGAGTGTGTAACCATGCTTTTCAC 246
Db 68 AlaseRAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 87
QY 247 TTCACATGCATCTCTCGTGGCTCAAAACACGACAGGTGTTCATTTGACACACAGAG 306
Db 88 PheHisCysIleSerArgTrpLeuYThrArgGlnValCysProLeuAspValCysGln 107
QY 307 TGGGAATTCCAAAGTATGGGCAC 330
Db 108 TrpGluPheGlnIleYTrpGlyHis 115

RESULT 4

T27823
hypothetical protein ZK287.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27823
R:McMurray, A.
Submitted to the EMBL Data Library, April 1996
A:Reference number: Z20425
A:Accession: T27823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-110 <WIL>
A:Cross-references: EMBL:Z70757, PIDN:CAA94801.1, GSPDB:GN00023, CESP:ZK287.5
A:Experimental source: clone ZK287
C:Genetics:
A:Gene: CESP: ZK287.5

A:Residues: 1-99 <DOU>
C:Cross-references: GB:A010592; NID:g12580758; PIDN:CAC27076.1; GSPDB:GN00151
A:Map position: 2
A:Genetics:
A:Genome: nucleomorph
C:Keywords: nucleomorph

Alignment Scores:

Pred. No.:	4.65e-06	Length:	99
Score:	132.50	Matches:	24
Percent Similarity:	52.78%	Conservative:	14
Best Local Similarity:	33.33%	Mismatches:	27
Query Match:	13.77%	Indels:	7
DB:	2	Gaps:	1

US-09-g14-3z4A-3 (1-508) x G90113 (1-99)

OY 124 GATAACTGTGCATTCGAGACCAATATGATCTTGGCATGATGCA----- 177
 |||||
DB 22 GTLPGCSALAIIECYAHRASNAHLEULUNSPASHALAPCAPAPHEGLUGLARG 41
 |||||
OY 178 -----CTPACCAGGCGTCCCTACTTCCAGAGAAGTGACTGTGCATG 222
 |||
DB 42 VALGIYLSSHSSERLYSASPHELEUASPINLESERYSAANCYSPEHELEALATYR 61
 |||
OY 223 GGAGCTGTAAACCATCTTTTCACCTTCACATGCACTCTCCCTGCTCAAACAGCACAG 282
 |||||
DB 62 GLIAYGCSGLYHSERFHEHLSLEULELCYSILLEGUANTRPLILELEUASNLVS 81
 |||||
OY 283 GTGTGTCCATTGGACAACAGAGCTGGGAATTCCAA 318
 |||||
DB 82 ASNCYSPROLEUCYSSEARGLLETTPVALTYRLIN 93
 |||||

RESULT 13
566831
probable membrane protein YOL134c - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein ROE129, hypothetical protein O0508
C:Species: *Saccharomyces cerevisiae*
C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C:Accession: S66831; S72033
R:Arino, J.; Casamayor, A.; Gamio, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas, C.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66814
A:Accession: S66831
A:Molecule type: DNA
A:Residues: 1-129 <ART>
A:Cross-references: EMBL:T74876; NID:g1420022; PID:g1420023; MIPS:YOL134C
A:Experimental source: strain S288C
R:Aldea, M.; Piderfilte, L.; Casas, C.; Casamayor, A.; Khalid, H.; Balcells, L.; Arino,
Yeast 12, 1053-1058, 1996
A>Title: Sequence analysis of a 12 801 bp fragment of the left arm of yeast chromosome X
protein and six other open reading frames.
A:Reference number: S72030; MID:g19051593; PMID:8896270
A:Accession: S72033
A>Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-129 <ALD>
A:Molecule type: DNA
A:Residues: 1-129 <ALD>
A:Cross-references: EMBL:X95465; NID:g1628437; PIDN:CAM64735.1; PID:g1628441
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
C:Genetics:
A:Cross-references: SGD:S0005494
A:Map position: 15L
A>Note: YOL134C
C/Superfamily: *Saccharomyces* probable membrane protein YOL134C
C/Keywords: transmembrane protein
F/41-57/Domain: transmembrane #status predicted <TM>

Alignment Scores:

Pred. No.:	9.67e-05	Length:	129
Score:	120.50 <td>Matches:</td> <td>34</td>	Matches:	34
Percent Similarity:	48.10% <td>Conservative:</td> <td>4</td>	Conservative:	4
Best Local Similarity:	43.04% <td>Mismatches:</td> <td>20</td>	Mismatches:	20
Query Match:	13.08% <td>Indels:</td> <td>21</td>	Indels:	21

```

DB: 2 Gaps: 3
US-09-914-324A-3 (1-508) x S66831 (1-129)

QY 197 GTAGCGGAGCGCTGTGATTGACATTCATATGCAAGAATTCATATGTGGTTCCGCG 138
DB 1 MetAlaphegIyTTP-----HisserMeth:sgIySerillelethpPheleuGln 17
QY 137 ATGGACAGGTATCAACCAATATCCAGGCGCCAGAGGGCTACTGATTCATTCACATTTC 78
DB 18 IleaAaGlnLenseRThAlaIleSerH:saBgInnaSaAlaThrlaIaHIsPheleu 37
QY 77 ACTTCAAAGCGCTTCTTGCCGCCGCCGCTGTGGTCCCGCGGTA-----30
DB 38 IleserAanLeuPhe-----PheleuValSerThrgIyAlaLeuTTPheGln 53
QY 29 -----TCCACATCGATCGTCCCGCATTTTG 3
DB 54 LeuCyAlaIlePheCyaspSerSerSerThrSerIleLeuSerThrSerLeu 72

RESULT 14
T20241
hypothetical protein H05L14.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 29-Oct-1999
C/Accession: T20241, T23049
R:Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z19241
A/Accession: T20241
A/Status: preliminary; translated from GB/EMBL/DDbU
A/Molecule type: DNA
A/Residues: 1-2160 <W12>
A/Cross-references: EMBL:Z75533; PIDN:CAA99823.1; GSPDB:GN00019; CESP:H05L14.2
A/Experimental source: clone C54G4
R:Barlow, K.
submitted to the EMBL Data Library, October 1997
A/Reference number: Z19662
A/Accession: T23049
A/Status: preliminary; translated from GB/EMBL/DDbU
A/Molecule type: DNA
A/Residues: 1-2160 <W12>
A/Cross-references: EMBL:Z99772; PIDN:CAB16922.1; GSPDB:GN00019; CESP:H05L14.2
A/Experimental source: clone H05L14
C/Genetics:
A/Gene: CESP:H05L14.2
A/Map position: 1
A/Introns: 49/3; 130/3; 190/3; 237/3; 290/1; 463/3; 507/1; 524/2; 545/1; 636/2; 663/2.

Alignment Scores:
Pred. No.: 0.000273 Length: 2160
Score: 116.50 Matches: 29
Percent Similarity: 42.11% Conservative: 11
Best Local Similarity: 30.53% Mismatches: 38
Query Match: 12.11% Gaps: 17
DB: 2 Gaps: 3

US-09-914-324A-3 (1-508) x T20241 (1-2160)

QY 28 GATACCCCGAGCGGCAACACAGCGCGCGGCAAGAGCGCTTGAAGTGAAAAAGTG 87
DB 2068 AspValPromeRProPheSerGluThrValMetLysLysMetPheGlnCySserGlyTyr 2087
QY 88 AATGCAGTAGCCCTCTGCGCTGAGTATTGTGGTT-----GATAACTGTGCATC 138
DB 2088 GluLeuAspValValThrgIuA:rgIuGluValValGluGluGluA:spGlyCysLeuIle 2107
QY 139 TCGAGAACCACTTATGATCTTGTGATGAAGAAGTCAAGTACACAGCGCTCGCTACT 198
DB 2108 Cys---ThrgIuIleIleGluGluAlaValGln-----2117
QY 199 TCAGAGAGTGTACTGCTCGCATGGGAGTGTGTAAACCATGCTTTTCATTCGACTGCATC 258
DB 199 TCAGAGAGTGTACTGCTCGCATGGGAGTGTGTAAACCATGCTTTTCATTCGACTGCATC 258

```

Db 2118 -----ThrValThrCysAspThrCysThrArgGluTyrHisTyrHisCysIle 2133
 QY 259 TCTGGCTGGCTCAAAACACAGACAGGTGTCTGCATTGGACACAGA 303
 |||||
 Db 2134 SerArgTTPLeuLysIleAsnSerValCysProGlnCysSerArg 2148
 |||||

RESULT 15

T06680

hypothetical protein T17F15.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000

C:Accession: T06680

R:Querier, F.; Choisme, N.; Robert, C.; Brotlier, P.; Wincker, P.; Cattolico, L.; Artigou

submitted to the Protein Sequence Database, April 1999

A:Reference number: 215793

A:Accession: T06680

A:Molecule type: DNA

A:Residues: 1-349 <QUE>

A:Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.100

A:Experimental source: cultivar Columbia; BAC clone T17F15

C:Genetics:

A:Gene: ATSP:T17F15.100

A:Map position: 3

A:Introns: 26/1; 81/2

C:Superfamily: RING finger homology

F:203-254/Domain: RING finger homology <RRN>

Alignment Scores:

Pred. No.:	0.00491	Length:	349
Score:	105.00	Matches:	23
Percent Similarity:	43.06%	Conservative:	8
Best local Similarity:	31.94%	Mismatches:	25
Query Match:	10.91%	Indels:	16
DB:	2	Gaps:	3

US-09-914-324a-3 (1-508) x T06680 (1-349)

QY 127 AACTGTGCATCTGCAGAAACACATTATGATCTTGCATAGATGCAAGCTAACAG 186
 |||||
 Db 206 AspCysAlaValCysLeuAsnGluPheSerAsp----- 216
 |||||
 QY 187 GCGTCCGCTACTTCAGAAAGTGTACTGTCGATGGGAGTCTGTACCATGCTTTTCAC 246
 |||||
 Db 217 -----ThrAspLysLeuArgLeu---ProValCysSerHisAlaPheHis 231
 |||||
 QY 247 TTGCACTGCATCTCTGCTGCTGCACAAACACAGAGTGTGCATTGGACAAACAGAGAG 306
 |||||
 Db 232 LeuHisCysIleAspThrTTPLeuLeuSerAsnSerThrCysProLeuCysArgArgSer 251
 |||||
 QY 307 TGGAAATTCCAAAG-----TATGGGCACTAGAAA 336
 |||||
 Db 252 LeuSerThrSerAsnValCysTyrAsnHisSerGlu 263
 |||||

Search completed: March 25, 2004, 09:24:24
 Job time : 19.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: March 25, 2004, 09:15:55 ; Search time 14 Seconds
(without alignment)

3778.806 Million cell updates/sec

Title: US-09-914-324A-3

Perfect score: 962
Sequence: 1 cccaataatgcgcagcagat.....aaagtcagtgatctctcg 508

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+np.model -DEV=xlp
-C=/cgn2.1/USPTO_epool_p/US09914324/runatc.25032004.090846.8718/app_query.fasta.1.647
-DB=SwissProt 42 -QPM=faolan -SUFFIX=esp -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NOM=ext -HEAPSIZE=500 -MINLEN=200000000
-USER=US09914324 @CCN 1.1.16 @runat 25032004.090846.8718 -NCPUS=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FAPOP=6
-FAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	64.0	108	1	RBX1_HUMAN
2	604	62.8	108	1	RBX1_SALSA
3	534	55.5	108	1	RBX1_DROME
4	514.5	53.5	118	1	RBX1_ARATH
5	499	51.9	115	1	RBX1_ARATH
6	493	51.2	110	1	RBX1_CAEEL
7	469	48.8	107	1	RBX1_SCHPO
8	400.5	41.6	122	1	RBX1_DROME
9	385	40.0	121	1	RBX1_YEAST
10	292	30.4	113	1	RBX2_HUMAN
11	290.5	30.2	113	1	RBX2_MOUSE
12	209	21.7	84	1	ANIL1_MOUSE
13	208	21.6	84	1	ANIL1_HUMAN
14	164.5	17.1	94	1	VIRP_SCHPO
15	91	9.5	148	1	RN12_HUMAN
16	90	9.4	600	1	RN12_MOUSE
17	88	9.1	161	1	YOUD_CAEEL
18	87	9.0	624	1	RN12_HUMAN

19	86	8.9	326	1	PEXA_HUMAN	Q06683 homo sapien
20	86	8.9	419	1	PEXA_PICPA	Q92265 pichia past
21	85.5	8.9	232	1	Z364_HUMAN	Q9Y415 homo sapien
22	85.5	9.3	474	1	KPY3_AGRVI	P70789 agrobacteri
23	84	8.7	796	1	PRH_ARATH	P48785 arabidopsis
24	83.5	8.7	115	1	YER2_YEAST	P38239 saccharomyc
25	83	8.6	279	1	SLI3_HUMAN	Q14192 homo sapien
26	83	8.6	488	1	RNF6_MOUSE	Q8Y556 mus musculu
27	83	8.6	585	1	RNF6_HUMAN	Q9Y552 homo sapien
28	82.5	8.6	532	1	ICP0_HSEVB	P28990 equine herp
29	82.5	8.6	547	1	YDRD_SCHPO	Q13747 schizosacch
30	80.5	8.7	3703	1	ABF1_HUMAN	Q15911 homo sapien
31	80.5	8.7	3726	1	ABF1_MOUSE	Q61329 mus musculu
32	80	8.3	284	1	GOLI_DROME	Q06003 drosophila
33	80	8.3	583	1	YORF_SCHPO	Q9P0E1 schizosacch
34	79.5	8.3	305	1	Z364_MOUSE	Q9P0E1 mus musculu
35	79.5	8.3	437	1	PROB_MOUSE	P11680 mus musculu
36	79.5	8.6	482	1	KPY4_AGRVI	Q44473 agrobacteri
37	79.5	8.6	1221	1	TOP2_TREYB	P12531 trypanosoma
38	79	8.2	381	1	RN13_CHICK	Q90972 gallus gall
39	79	8.2	381	1	RN13_HUMAN	Q43567 homo sapien
40	79	8.2	381	1	RN13_MOUSE	Q54965 mus musculu
41	79	8.2	410	1	ICP0_PRRVT	P29129 pseudorabie
42	79	8.2	1679	1	FUR2_DROME	P30432 drosophila
43	78.5	8.2	235	1	YQ57_CAEEL	Q09463 caenorhabd
44	77.5	8.1	1493	1	M3K1_MOUSE	P53349 mus musculu
45	77	8.0	295	1	PEXA_PICPA	Q00940 pichia angu

ALIGNMENTS

RESULT 1
RBX1_HUMAN STANDARD; Q9Y254; PRT; 108 AA.
ID RBX1_HUMAN
AC Q86628; Q9D1S2; Q9WUK3; Q9Y254;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 43, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1 (Rbx1) (Regulator of cullins 1) (RING finger
protein 75) (zyp protein).
GN RBX1 OR ROCI OR RNF75.
OS Homo sapiens (Human), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606, 10090.
RN [1]
RP SEQUENCE FROM N.A., INTERACTION WITH CULLINS, AND MUTAGENESIS OF
CYS-53; CYS-56; CYS-75 AND HIS-77.
RC SPECIES=Human; TISSUE=Cervical carcinoma;
RX MEDLINE=99247022; PubMed=10230407;
RA Ohta T., Michel J.U., Schottelius A.J., Xiong Y.,
RT "ROCI, a homolog of Apcl1, represents a family of cullin partners with
an associated ubiquitin ligase activity.";
RL Mol. Cell 3:535-541(1999).
RV [2]
RP SEQUENCE FROM N.A., AND IDENTIFICATION IN CBC(VHL) COMPLEX.
RC SPECIES=Human, and Mouse;
RX MEDLINE=99234320; PubMed=10213691;
RA Kamura T., Koepf D.M., Conrad M.N., Skowrya D., Moreland R.J.,
RA Iliopoulos O., Lane W.S., Kaelin W.G. Jr., Ellledge S.J., Conway R.C.,
RA Harper J.W., Conaway J.W.;
RT "Rbx1, a component of the VHL tumor suppressor complex and SCF
ubiquitin ligase.";
RL Science 284:657-661(1999).
RV [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clamp M., Smink L.J., Alnecough R.F., Almeida J.P., Babbage A.K.,
RA Bagdely C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

RA Burdell W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis U., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leverhulme M.A., Lloyd C., Lloyd D.M.,
RA Marlyn I.D., Matherly S.A., Matthews L.H., McLean O.T.,
RA McElroy J., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.J.C.T.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vandin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malai E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chiswick S., Murray J., Miller N., Mink P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozeresky P., Roffling T.,
RA Schreier P., Malker C., Mameli A., Mohlmann P., Pepin K., Nelson J.,
RA Kofler I., Bedell U.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
RA Budarf M.L., McEldermott H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumas J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Butler C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliakou Y., Wright H.,
RA "The DNA sequence of human chromosome 22.",
RA Nature 402:489-495(1999).
[4]
RA SEQUENCE FROM N.A.
RA SPECIES=Human, and Mouse; TISSUE=Brain, Mammary gland, and Placenta;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Collins P.S., Wagner L.H., Shenman C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Nak S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Mulvaney S.J.,
RA Rabe S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullany S.W.,
RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.",
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RA SEQUENCE FROM N.A.
RA SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Embryo;
RA MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikiado I., Oseto N., Saito R., Suzuki H., Yamana T., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Drisanti T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
RA Grammett S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kani A., Kawaji H., Kawasawa Y., Kedzierski R.M., King P.A.,
RA Kongstad D.R., Kurochkin I.V., Lee Y., Lehman B., Lyons P.A.,
RA Maglott D.R., Maltz L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sulana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilting L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Zimmet P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.",
RA Nature 420:563-573(2002).
[6]
RA SEQUENCE OF 14-108 FROM N.A.
RA SPECIES=Human, TISSUE=Brain;
RA MEDLINE=20106778; PubMed=10643962;
RA Perin U.-P., Seddighi N., Chattermeyer F., Goudou D., Belkadi L.,
RA Rieger F., Allier P.M.,
RA "Genomic organization and expression of the ubiquitin-proteasome
RA complex-associated protein Rbx1/ROCI1/Hrt1",
RA Cell. Mol. Biol. 45:1131-1137(1999).
[7]
RA SEQUENCE OF 92-105, INTERACTION WITH CUL1, AND
RA IDENTIFICATION IN A COMPLEX WITH CUL1, SKP1 AND SKP2.
RA SPECIES=Human; TISSUE=Cervical carcinoma;
RA MEDLINE=99247021; PubMed=10230406;
RA Tan P., Fuchs S.Y., Chen A., Wu K., Gomez C., Ronai Z., Pan Z.-Q.,
RA "Recruitment of a ROCI1-CUL1 ubiquitin ligase by Skp1 and HOS to
RA catalyze the ubiquitination of I kappa B alpha.",
RA Mol. Cell Biol. 19:527-533(1999).
[8]
RA FUNCTION.
RA SPECIES=Human;
RA MEDLINE=20047893; PubMed=10579999;
RA Kamura T., Conrad M.N., Yan Q., Conaway R.C., Conaway J.W.,
RA "The Rbx1 subunit of SCF and VHL E3 ubiquitin ligase activates Rbx1
RA modification of cullins Cdc53 and Cul2.",
RA Genes Dev. 13:2928-2933(1999).
[9]
RA FUNCTION, AND SUBCELLULAR LOCATION.
RA SPECIES=Human;
RA MEDLINE=20481777; PubMed=11027288;
RA Furukawa M., Zhang Y., McCarville J., Ohta T., Xiong Y.,
RA "The Cul1 C-terminal sequence and ROCI are required for efficient
RA nuclear accumulation, NED8 modification, and ubiquitin ligase
RA activity of Cul1.",
RA Mol. Cell Biol. 20:8185-8197(2000).
[10]
RA IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MUF1, AND
RA IDENTIFICATION IN COMPLEXES WITH CUL5.
RA SPECIES=Human, and Mouse;
RA MEDLINE=21380117; PubMed=11384984;
RA Kamura T., Burian D., Yan Q., Schmidt S.L., Lane W.S., Querido E.,
RA Branton P.E., Shilatifard A., Conaway R.C., Conaway J.W.,
RA "Muf1, a novel elongin Bc-interacting leucine-rich repeat protein
RA that can assemble with Cul5 and Rbx1 to reconstitute a ubiquitin
RA ligase.",
RA J. Biol. Chem. 276:29748-29753(2001).
[11]
RA IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MED8.
RA SPECIES=Human;
RA MEDLINE=22155962; PubMed=12149480;

RA Brower C.S., Sato S., Tomomori-Sato C., Kamura T., Pause A.,
 RA Stearns R., Klausner R.D., Malik S., Lane W.S., Sorokina I.,
 RA Roeder R.G., Conway J.W., Conway R.C.,
 RT "Mammalian mediator subunit mMED8 is an Elongin Bc-interacting protein
 RT that can assemble with Cul2 and Rbx1 to reconstitute a ubiquitin
 RT ligase."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:10353-10358(2002).
 RN [12]
 RP IDENTIFICATION IN SCF-LIKE COMPLEX, AND INTERACTION WITH CUL7.
 RP SPECIES=Human;
 RX MEDIAN=22388271; PubMed=12481031;
 RA Dias D.C., Dolios G., Wang R., Pan Z.Q.,
 RT "CUL7: A DCC domain-containing cullin selectively binds Skp1.Fbx29 to
 RT form an SCF-like complex.";

Alignment Scores:

Pred. No.: 2,23e-59 Length: 108
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.03% Indels: 0
 DB: 1 Gaps: 0

US-09-914-324A-3 (1-508) x RBX1_HUMAN (1-108)

QY 7 ATGGCGGCGCGCATGATGATGATACCCCGAGCGGCAACAGCGGCGGCAAGAG 66
 DB 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 QY 67 CGCTTTGAAGTGAAGAAAGAGTGAATGCAGTACGCTCTGGGCTGGGATATTGGTTGAT 126
 DB 21 ArgPheGluValLysLysLysTrpAsnAlaValAlaLeuThrPalaTrpAspIleValAlaLys 40
 QY 127 AACTGTGCATCTGCAGAGACCAATATGATCTTTTGCATGATTCACACTTACAG 186
 DB 41 AsnCySaAlaIleCysAspAsnHisIleMetAspLeuCyIleGluCysGlnAlaAsnGln 60
 QY 187 GGGTCGGCTACTTGCAGAGAGTGTACTGTGCGAGTGGGAGTGTGAACATCTTTTAC 246
 DB 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisIleAsnHis 80
 QY 247 TTCACATGATCTCTGCTGCTGCTCAAAACAGACAGAGTGTGCATTCAGACACAGAG 306
 DB 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGln 100
 QY 307 TGGGAATTCGCAAAAGATGGGAC 330
 DB 101 TrpGluPheGlnLysTrpGlyHis 108
 RESULT 2
 RBX1_SALSA STANDARD; PRT; 108 AA.
 ID RBX1_SALSA
 AC 08064;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein 1 (Rbx1) (Hyperosmotic protein 21).
 OS RBX1 OR SHOB21.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proteobacteria; Salmoniformes; Salmonidae; Salmo.
 OC NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION.
 RP TISSUE=Gill;
 RX MEDLINE=22005592; PubMed=12010746;
 RA Pan F., Zarate J., Bradley T.M.,
 RT "A homolog of the E3 ubiquitin ligase Rbx1 is induced during
 RT hyperosmotic stress of salmon."
 RT Am. J. Physiol. 282:R1643-R1653(2002).
 CC -!- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC ubiquitin ligase complex, which mediates the ubiquitination and

CC subsequent proteasomal degradation of target proteins. Through the
 CC RING-type zinc finger, seems to recruit the E2 ubiquitination
 CC enzyme, like CDC34, to the complex and brings it into close
 CC proximity to the substrate (By similarity).
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Part of SCF complexes, which consist of SKP1, CUL1,
 CC RBX1 and a F-box protein (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in heart and kidney.
 CC -!- INDUCTION: During hyperosmotic stress and thermal stress.
 CC -!- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -!- SIMILARITY: Belongs to the RBX1 family.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AY027936; AAK29182.1; ALT_INIT.

DR InterPro; IPR001841; ZnF_Ring.

DR Pfam; PR00097; ZF-C3HC4_1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PSS0089; ZF_RING_2; 1.

KM Ub1 conjugation pathway; Nuclear protein; Zinc; Zinc-finger;

KT Metal-binding.

FT ZN FING 53 98

FT METAL 42 42

FT METAL 45 45

FT METAL 53 53

FT METAL 56 56

FT METAL 68 68

FT METAL 75 75

FT METAL 77 77

FT METAL 80 80

FT METAL 82 82

FT METAL 83 83

FT METAL 94 94

FT METAL 97 97

SQ SEQUENCE 108 AA; 12318 MM; 44CB3A712C8D7BB CRC64;

Alignment Scores:

Pred. No.: 4.61e-58 Length: 108
 Score: 604.00 Matches: 106
 Percent Similarity: 98.15% Conservative: 0
 Best Local Similarity: 98.15% Mismatches: 2
 Query Match: 62.79% Indels: 0
 DB: 1 Gaps: 0

US-09-914-324A-3 (1-508) x RBX1_SALSA (1-108)

QY 7 ATGGCGGCGCGCATGATGATGATACCCCGAGCGGCAACAGCGGCGGCAAGAG 66
 DB 1 MetAlaAlaAlaMetAspValAspThrProSerAlaThrAsnSerGlyAlaSerLysLys 20
 QY 67 CGCTTTGAAGTGAAGAAAGAGTGAATGCAGTACGCTCTGGGCTGGGATATTGGTTGAT 126
 DB 21 ArgPheGluValLysLysLysTrpAsnAlaValAlaLeuThrPalaTrpAspIleValAlaLys 40
 QY 127 AACTGTGCATCTGCAGAGACCAATATGATCTTTTGCATGATTCACACTTACAG 186
 DB 41 AsnCySaAlaIleCysAspAsnHisIleMetAspLeuCyIleGluCysGlnAlaAsnGln 60
 QY 187 GGGTCGGCTACTTGCAGAGAGTGTACTGTGCGAGTGGGAGTGTGAACATCTTTTAC 246
 DB 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisIleAsnHis 80
 QY 247 TTCACATGATCTCTGCTGCTGCTCAAAACAGACAGAGTGTGCATTCAGACACAGAG 306

Db 81 Pheh1Cys15Ser1Agt1Ple1Lys1Thr1Arg1Val1Cys1Pro1Leu1Asp1Arg1Glu 100
 Oy 307 TGGGAATTCCTCAAGATGAGGAC 330
 Db 101 Ttp1uph1es1ln1y1ty1g1/h1s 108

RESULT 3
 RBXA DROME STANDARD; PRT; 108 AA.
 ID RBXA DROME
 AC Q9W5E1; 077429;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein 1A (Regulator of cullins 1a) (drrx1).
 GN RING-BOX OR CG16982 OR EG:115C2.11.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelecygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_Taxid:7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards B., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blake J.R.G., Chape M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abri1 J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benise P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
 RA Burris K.C., Busan D.A., Butler J., Brockstein P., Brodtier P.,
 RA Chert J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Galbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kenson J.A., Ketchum K.A.,
 RA Khatami B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Misha N.V., Moberg C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski W.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E.,
 RA Barrett B.G., Ferraz C., Vidal S., Brun C., Demallies J., Brokova D.,
 RA Drees S., Glouf S., Lelaure V., Mottier S., Galibert F., Borokova D.,
 RA Minna B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papadogiannakis G., Spanos L., Cox S., Meduno E., de Pablos B.,
 RA Modolelli J., Peter A., Schoettler P., Werner M., Mourkioti F.,
 RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A., S.,
 RA Callister D.M., Campbell L.A., Darlantisou A., Henderson N.S.,
 RA McMillan P.J., Sallies C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 RT melanogaster.";
 RL Science 287:2220-2222(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley; TISSUE=Embryo;
 RX MEDLINE=2242606; PubMed=12537569;
 RA Stapleton M., Carlson U.W., Brokstein P., Yu C., Chape M.,
 RA George R.A., Guarini H., Krommiller B., Pauley J.M., Park S., Wan K.H.,
 RA Rubin G.M., Ceiniker S.E.;
 RT "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 RN [4]
 RP FUNCTION, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTAGENESIS OF
 RP ASN-59 AND CYS-68.
 RX MEDLINE=22057626; PubMed=12062088;
 RA Noureddine M.A., Donaldson T.D., Thacker S.A., Duronio R.J.,
 RA Drosophila Roca encodes a RING-H2 protein with a unique function in
 RT processing the Hh signal transducer Ci by the SCF E3 ubiquitin
 RT ligase.";
 RL Dev. Cell 2:757-770(2002).
 RN [5]
 RP INTERACTION WITH LIN19 AND SLMB.
 RX MEDLINE=21391618; PubMed=11500045;
 RA Bocca S.N., Muzopappa M., Silberstein S., Wapner P.;
 RT "Occurrence of a putative SCF ubiquitin ligase complex in
 RT Drosophila.";
 RL Biochem. Biophys. Res. Commun. 286:357-364(2001).
 RN [6]
 RP REVIEW ON E3 UBIQUITIN LIGASE COMPLEXES.
 RX MEDLINE=2273611; PubMed=12850443;
 RA Ou C.-Y., Pi H., Chien C.-T.;
 RT "Control of protein degradation by E3 ubiquitin ligases in Drosophila
 RT eye development.";
 RL Trends Genet. 19:382-389(2003).
 RN [7]
 RP FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC ubiquitin ligase complex, which mediates the ubiquitination and
 CC subsequent proteasomal degradation of target proteins. Through the
 CC RING-type zinc finger, seems to recruit the E2 ubiquitination
 CC enzyme to the complex and brings it into close proximity to the
 CC substrate. Required for the specific SCF-dependent proteolysis of
 CC Ct, but not that of Abm, suggesting that it also participates in
 CC the selection of substrates inside the SCF complex.
 CC -1- SUBUNIT: Part of a SCF complex consisting of SkpA (SKP1), Lin19
 CC (CUL1), Roc1A and F-box protein Slmb. Interacts directly with
 CC Lin19 and Slmb.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Widely expressed. Expressed in embryonic,
 CC larval and adult tissues.
 CC -1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom (By similarity).
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL; AE003418; AAF55536.1;
 CC EMBU; AL031581; CAA20888.1; ALT_SEQ.

RP CUL1 AND TIR1, AND INTERACTION WITH CUL1.
 RX MEDLINE=22204438; PubMed=12215511;
 RA Gray W.M., Hellmann H., Dharmasiri S., Estelle M.;
 RT "Role of the Arabidopsis RING-H2 protein RBX1 in RUB modification and
 SCF function.";
 RL Plant Cell 14:2137-2144 (2002).
 RN [7]
 RP FUNCTION. TISSUE SPECIFICITY. IDENTIFICATION IN SCF COMPLEX, AND
 RP INTERACTION WITH CUL1, CUL4, ASK1 AND ASK2.
 RX MEDLINE=22370998; PubMed=12387738;
 RA Lechner E., Xie D., Grava S., Pisaggio E., Planchais S.,
 RA Murray J.A.H., Parmentier Y., Mutterer J., Dubreucq B., Shen W.-H.,
 RA Genschik P.;
 RT "The AtRbx1 protein is part of plant SCF complexes, and its
 RT down-regulation causes severe growth and developmental defects.";
 RL J. Biol. Chem. 277:50065-50080 (2002).
 RN [8]
 RP FUNCTION.
 RX MEDLINE=22568282; PubMed=12682009;
 RA Dharmasiri S., Dharmasiri N., Hellmann H., Estelle M.;
 RT "The RUB/RBX1 conjugation pathway is required for early development
 RT in Arabidopsis.";
 RL EMO J. 22:1762-1770 (2003).
 CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC subsequent proteasomal degradation of target proteins. The SCF
 CC complex plays a crucial role in regulating response to auxin and
 CC is essential for growth and development. Through the RING-type
 CC zinc finger, seems to recruit the E2 ubiquitination enzyme, to the
 CC complex and brings it into close proximity to the substrate.
 CC Promotes the neddylation of CUL1.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of SCF complexes, which consist of a SKP1-related
 CC protein, a cullin, a RBX protein and a F-box protein. Part of a
 CC SCF complex with ASK1 or ASK2 and CUL1. Part of a SCF complex with
 CC CUL1 and TIR1. Interacts with CUL1 and CUL4.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Widely expressed. Expressed in shoot, leaves,
 CC siliques, meristem, flowers, floral buds, open flowers, leaves,
 CC stems, roots, germinal seeds and seedlings in dark. Expressed at a
 CC higher level in tissues containing actively dividing cells.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AY052401; AAL13435.1; -
 CC EMBL; AF296833; -; NOT ANNOTATED_CDS.
 CC EMBL; AY086913; AAM64477.1; -
 CC EMBL; AY072430; AAL62422.1; -
 CC EMBL; AY114719; AAM48038.1; -
 CC EMBL; AK118181; BAC42804.1; -
 CC InterPro: IPR001841; Znf_ring.
 CC Pfam: PF00097; zf-C3HC4_1.
 CC PROSITE: PS50089; ZF_RING_2_1.
 CC Ubl conjugation pathway; Nuclear protein; Zinc; zinc-finger;
 KM Metal-binding.
 FT ZN FING 63 108 RING-TYPE.
 FT METAL 52 52 ZINC 1 (BY SIMILARITY).
 FT METAL 55 55 ZINC 1 (BY SIMILARITY).
 FT METAL 63 63 ZINC 3 (BY SIMILARITY).
 FT METAL 66 66 ZINC 3 (BY SIMILARITY).
 FT METAL 78 78 ZINC 3 (BY SIMILARITY).
 FT METAL 85 85 ZINC 2 (BY SIMILARITY).

FT METAL 87 87 ZINC 2 (BY SIMILARITY).
 FT METAL 90 90 ZINC 1 (BY SIMILARITY).
 FT METAL 92 92 ZINC 3 (BY SIMILARITY).
 FT METAL 93 93 ZINC 1 (BY SIMILARITY).
 FT METAL 104 104 ZINC 2 (BY SIMILARITY).
 FT METAL 107 107 ZINC 2 (BY SIMILARITY).
 SC SEQUENCE 118 AA; 13238 MW; 19947BF06F442A82 CRC64;
 Alignment Scores:
 Pred. No.: 2,99e-48 Length: 118
 Score: 514.50 Matches: 92
 Percent Similarity: 83.76% Conservative: 6
 Best Local Similarity: 78.63% Mismatches: 8
 Query Match: 53.48% Indels: 11
 DB: 1 Gaps: 2
 US-09-914-324a-3 (1-508) x RBX1_ARATH (1-118)
 QY 13 GCAGCGATGATGTGATAC-----CCGAGCGC----- 42
 Db 2 AATATLAApSPserASpvalThmCtLleProAlagLgAlaSerSeValaLa 21
 QY 43 ---ACCAACAGCGCGCGCGCAGAGAGCGCTTTGAGTGAAGAAAGTGAATGACATGCC 99
 Db 22 AlaSerSeValenLylValAlaLylsghGguLleLylsLSTpSerAlaValaLa 41
 QY 100 CTTGCGGCTGGGATATTTGGTTGATTAATGATGTCATCTGCAGGACACATTTATGAT 159
 Db 42 LeuTPAATpASpLleValaValaSpasnCySAAlaLleCyASpASpNHleleVasp 61
 QY 160 CTTTCATAGATATGTCACAGTCAACGAGCGGCTGCTACTTACAGAAAGTACTGTCCGA 219
 Db 62 LeuCySllleGlyCyGlnAlaLsnGlnAlaSerAlaThrSerGluGluCyThValaLa 81
 QY 220 TGGGAGTGTGTACCATCTTTTCACTTCCATGTCATCTCTCGTGGCTCAAAACAGCA 279
 Db 82 TTPGilyValCyASpNHleAlaAlaPheHisPheHisCySllleSerArASpTrpLeuLysThArG 101
 QY 280 CAGGTGTGTCCATTGGACACACAGAGAGTGGGATTCGAAAGTATGCGGCAC 330
 Db 102 GlnValCySProlenASpASpSerGluTrpGluPheGlnLysTrpGlyHis 118
 RESULT 5
 RBX1_ARATH STANDARD; PRT; 115 AA.
 AC QPM250;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DE Putative RING-box protein 1b (RBX1b-Ac) (At-Rbx1/2) (RBX1-1).
 GN RBX1b OR AT3G42830 OR T21C14.50.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OC NCBI_TaxID=3702;
 RX MEDLINE=21016720; PubMed=1130713;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Salasoubat M., Lencake K., Rieger M., Ansgore W., Unseid M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Deiseny M., Boutry M., Givelli L.A., Macho R., Puldomenech P.,
 RA De Simone V., Choiso L., Artiguenave F., Robert C., Brotlier P.,
 RA Wincker P., Cattoiolo N., Weissenbach J., Saurin W., Queller F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wuerbach E., Drzozek H., Ertle H., Jordan N., Bangert S.,
 RA Niedeilmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelico M., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer O., Joehner T.H., Nordstiek G.,
 RA Reichelt J., Scharte M., Schoen O., Barges M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwalder B., Ducheman D.,
 RA Cooke R., Landie M., Berger-Llauro C., Purnelle B., Masny D.,

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FT METAL 82 82 ZINC 2 (BY SIMILARITY)
FT METAL 84 84 ZINC 2 (BY SIMILARITY)
FT METAL 87 87 ZINC 1 (BY SIMILARITY)
FT METAL 89 89 ZINC 3 (BY SIMILARITY)
FT METAL 90 90 ZINC 1 (BY SIMILARITY)
FT METAL 101 101 ZINC 2 (BY SIMILARITY)
FT METAL 104 104 ZINC 2 (BY SIMILARITY)
SQ SEQUENCE 115 AA; 12999 MW; 1515E3E417DE1FAF CRC64;

Alignment Scores:
Pred. No.: 1,486-46 Length: 115
Score: 499.00 Matches: 88
Percent Similarity: 86.11% Conserved: 5
Best Local Similarity: 81.48% Mismatches: 13
Query Match: 51.87% Indels: 2
DB: 1 Gaps: 1

US-09-914-324A-3 (1-508) x RBXB_ARATH (1-115)
QY 7 ATGGCGCGGACCATGATGGATATACCCCGAGCGGACACAGCGGCGCGGACAGAG 66
Db 10 MetGLyGluSerSerSerLeuValProSer-----SerSerLyAsnSerLyS 27
QY 67 CGGTTTGAGATGAAAAGATGAAATGACATACCCCTCTGGGCGCTGGATATTGGTGAT 126
Db 28 ArgPheGluLeuLeuLeuTrpSerLeuAlaLeuTrpAlaLeuTrpAlaLeuValAsp 47
QY 127 AACTGTGCATCTGCAGACACCACTTTATGATCTTTGCATGAAATGCAAGCTAACCA 166
Db 48 AsnCyAlaIleCysArgSerHisIleMetAspLeuCyIleGluCysLeuAlaAsnGln 67
QY 187 GCGTCGCGACTTCGAGAGAGTACTGCGATGGGAGGCTGTAAACATGCTTTTCAC 248
Db 68 AlSerLeuAlaThrSerGluGluCysThrValaIleTrpGlyValCysAsnHisAlaPheHis 87
QY 247 TTCACATGATCTCTGCTGCTGCTCAAAAACAGCAGCGTGTGTCCATTGGACACAGGAG 306
Db 88 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspValCysGlu 107
QY 307 TGGGAATTCGAAAAGATGAGGAG 330
Db 108 TrpGluPheGluIleuTyrgIyHis 115

RESULT 6
RBX1_CABEL STANDARD; PRT; 110 AA.
ID RBX1_CABEL.
AC Q23457; Q8WSQ1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RING-box protein 1 (Rbx1) (Ce-rbx-1).
GN RBX-1 OR ZK287.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderrinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol NZ;
RA McMurtry A.A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RN SEQUENCE OF 2-110 FROM N.A.
RA Saegawa Y., Urano T., Kohara Y., Takahashi H., Higashitani A.;
RA "Characterization of rbx1 gene from Caenorhabditis elegans."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL - FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
CC ubiquitin ligase complex, which mediates the ubiquitination and
CC subsequent proteasomal degradation of target proteins. Through the
CC RING-type zinc finger, seems to recruit the E2 ubiquitination
CC enzyme to the complex and brings it into close proximity to the
CC substrate (By similarity).
CC -I- PATHWAY: Ubiquitin conjugation; third step.

```


CC RA Strausber R.L., Collings E.A., Grouse L.H., Derge J.G.,
CC RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
CC RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
CC RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang Y., Hsieh F.,
CC RA Diatchenko L., Marziska K., Farmer A.A., Rubin G.M., Hong L.,
CC RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant I.P., Scheetz T.E.,
CC RA Brownstein M.J., Udell T.B., Yoshiyuki S., Carninci P., Prange C.,
CC RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
CC RA Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
CC RA Richards S., Worley K.C., Hale S., Garcia A.L., Gay L.J., Huylk S.W.,
CC RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CC RA Fahey J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
CC RA Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,
CC RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
CC RA Buterfield Y.S.N., Krzywinski M.I., Skalka U., Smalins D.E.,
CC RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
CC RT "Generation and initial analysis of more than 15,000 full-length
CC human and mouse cDNA sequences".
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC
CC RL
CC RN INTERACTION WITH CUL1, AND FUNCTION.
CC RP MEDLINE=20305866; PubMed=10851089;
CC RX Swarcop W., Wang Y., Miller P., Duan H., Jatkeo T., Madore S.J.,
CC RA Sun Y.;
CC RT "Yeast homolog of human SAG/RCC2/Rbx2/Hrt2 is essential for cell
CC growth, but not for germination: chip profiling implicates its role
CC in cell cycle regulation";
CC Oncogene 19:2855-2866(2000).
CC
CC RL
CC RN PHOSPHORYLATION BY CK2.
CC RP MEDLINE=22765595; PubMed=12748192;
CC RX Kim Y.-S., Lee J.-Y., Son M.-Y., Park W., Bae Y.-S.,
CC RT "Phosphorylation of threonine 10 on CXBP1/SAG/RCC2/Rbx2 by protein
CC kinase CKI promotes the degradation of IkappaBalpha and p27kip1.";
CC RL Biol. Chem. 278:28462-28469(2003).
CC
CC RL
CC RN -FUNCTION: Probable component of the SCF (SKP1-CUL1-F-box protein)
CC E3 ubiquitin ligase complex which mediates the ubiquitination and
CC subsequent proteasomal degradation of target proteins involved in
CC cell cycle progression, signal transduction and transcription.
CC Through the RING-type zinc finger, seems to recruit the E2
CC ubiquitination enzyme to the complex and brings it into close
CC proximity to the substrate. May play a role in protecting cells
CC from apoptosis induced by redox steps.
CC
CC CC -PATHWAY: Ubiquitin conjugation; third step.
CC
CC CC -SUBUNIT: Probable part of SCF complexes, which consist of SKP1,
CC CUL1, RNF4/RBX2 and a F-box protein. Interacts with CUL1, CUL2,
CC CUL3, CUL4A, CUL4B and CUL5. Interacts with CSNK2B, the
CC interaction is not affected by phosphorylation by CK2.
CC
CC CC -SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC
CC CC -ALTERNATIVE PRODUCTS:
CC
CC CC Name=1;
CC IsoId=GQUBFc-1; Sequence=Displayed;
CC Name=2; Synonyms=SAC-V;
CC IsoId=GQUBFc-2; Sequence=VSP_008449;
CC Note=inactive;
CC
CC CC -TISSUE SPECIFICITY: Expressed in heart, liver, skeletal muscle and
CC pancreas. At very low levels expressed in brain, placenta and
CC lung.
CC
CC CC -INDUCTION: By 1,10-phenanthroline.
CC
CC CC -DOMAIN: The RING-type zinc finger domain is essential for
CC ubiquitin ligase activity. It coordinates an additional third zinc
CC atom.
CC
CC CC -PTM: Phosphorylation by CK2 is required for efficient degradation
CC of NFkBIA and CDKN1B.
CC
CC CC -SIMILARITY: Belongs to the RING-box family.
CC
CC CC -SIMILARITY: Contains 1 RING-type zinc finger.
CC
CC CC -----
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DR EMBL/ AF164679; AAD55984.1; -
DR EMBL/ AF142060; AAD30147.1; -
DR EMBL/ AF092878; AAD25962.1; -
DR EMBL/ AT112252; AAK37450.1; -
DR EMBL/ BT100748; AAP36012.1; -
DR EMBL/ BC005966; AAH05966.1; -
DR EMBL/ BC008627; AAH08627.1; -
DR MIM/ 603863; -
DR InterPro; IPR001841; Znf_xing.
DR Pfam; PF000097; zf-C3HC4; 1.
DR SMART; SW00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Ubl conjugation pathway; Zinc; Zinc-finger; Metal-binding;
KW Phosphorylation; Alternative splicing.
FT ZN FING 61 103
FT METAL 50 50
FT METAL 53 53
FT METAL 61 61
FT METAL 64 64
FT METAL 73 73
FT METAL 80 80
FT METAL 82 82
FT METAL 85 85
FT METAL 87 87
FT METAL 88 88
FT METAL 98 99
FT METAL 102 102
FT MOD_RES 10 10
FT VASPLIC 60 113
SQ CONFLICT 23 22
FT SEQUENCE 113 AA; 12683 MW; CEEB6AC940C8257 CRC64;
Alignment Scores:
Pred. No.: 7.05e-24
Score: 292.00
Percent Similarity: 64.95%
Best Local Similarity: 50.52%
Query Match: 30.35%
DB: 1
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QY 37 AGCGGACCAACAGCGGCGGCGGCAAGAACGCTTTGAAGTGAAGAAAAGTGAATGCAGTA 96
   |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 20 SerGlySerIlySerGly--GlyAspIlySmetPheSerLeuIlyStryPAspAlaVal 38
QY 97 GCCCTTCGGGCGCTGGATATGTGGTTGTAACGTGGCACTCGAGGAAACCATATATG 156
   |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 39 AlaMetTyrPheIrrPaspValIuGlyCyAspPrrIrcySaIalleCySArgValaGlnValMet 58
QY 157 GATCTTTCGATAGATGTCAAGATTAACCAAGCGCGTCGCTACTCTTCGAAAGAGTGAATGTC 216
   |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 59 AspAlaCySbeuAArgCySgIlnaIaGuAn-----LysGlnGlnAspCySValVal 75
QY 217 GCATGGGAGAGCTCTTAACCACTGCTTTTCACTTCCACTGCATGCATGCTCGGTGCTCAAAACA 276
   |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 76 ValTrpGlyIuGlySaAnHIsSerPheHIsaErCyCySmetSerLeuTrpValIlySgln 95
QY 277 GCAGAGGTGTCTTCATTTGAGCAACAAGAGAGTGGGATTTCCAAAAGTATGGG 327
   |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 96 AsnaAsnArgCySproLeuCySglnGlnaAspTrpValaGlnArgIleGly 112
RESULT 11
RBX2_MOUSE
ID RBX2_MOUSE STANDARD; PRT; 113 AA.
AC GAWT21;

```


GN ANAPC11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND SUBCELLULAR
 RP LOCATION.
 RX MEDLINE=21456959; PubMed=11573742;
 RA Chan A.H., Lee S.M.Y., Chim S.S., Kok L.D., Waye M.M.Y., Lee C.Y.,
 RA Fung K.P., Tsui S.K.W.,
 RT "Molecular cloning and characterization of a RING-H2 finger protein,
 RT ANAPC11, the human homolog of yeast Apclp1";
 RL J. Cell. Biochem. 83:249-258(2001).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Li N., Wan T., Zhang W., Cao X.;
 RT "Novel human APC11 anaphase-promoting complex subunit";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20499367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong W., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao Y., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-U., Chen Z.,
 RT "Cloning and functional analysis of CDNs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells";
 RL Genome Res. 10:1546-1560(2000).
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donaldson W.F., Caesvant I.L., Schetz T.E.,
 RA Brownstein M.J., Utsid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.D., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RP IDENTIFICATION IN APC/C COMPLEX.
 RX MEDLINE=20381321; PubMed=10922056;
 RA Gachul M., Gleffers C., Podtelejnikov A.V., Mann M., Peters J.-M.;
 RT "The RING-H2 finger protein APC11 and the E2 enzyme UBC4 are
 RT sufficient to ubiquitinate substrates of the anaphase-promoting
 RT complex";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:8973-8978(2000).
 [6]
 RP FUNCTION, MUTAGENESIS, AND INTERACTION WITH ANAPC2 AND UBE2D2.
 RX MEDLINE=21602823; PubMed=11739784;
 RA Tang Z., Li B., Bharadwaj R., Zhu H., Ozkan E., Hakala K.,
 RA Deisenhofer J., Yu H.;
 RT "APC2 cullin protein and APC11 RING protein comprise the minimal
 RT ubiquitin ligase module of the anaphase-promoting complex";
 RL Mol. Biol. Cell 12:3839-3851(2001).
 CC -1- FUNCTION: Component of the anaphase promoting complex/cyclosome
 CC (APC/C), a cell cycle-regulated E3 ubiquitin ligase that controls
 CC progression through mitosis and the G1 phase of the cell cycle.

CC May recruit the E2 ubiquitin-conjugating enzymes to the complex.
 CC -1- PATHWAY: Ubiquitin-conjugation, third step.
 CC -1- SUBUNIT: The APC/C is composed of at least 11 subunits. Interacts
 CC with the cullin domain of ANAPC2. Interacts with UBE2D2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9NMG5-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9NMG5-2; Sequence=VSP_008450;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Expressed at high levels in skeletal muscle
 CC and heart; in moderate levels in brain, kidney, and liver; and at
 CC low levels in colon, thymus, spleen, small intestine, placenta,
 CC lung and peripheral blood leukocyte.
 CC -1- DOMAIN: The RING-type zinc finger domain coordinates an additional
 CC third zinc atom.
 CC -1- PPM: Auto-ubiquitinated.
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 67.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sb-sib.ch).
 CC -----
 CC EMBL: AF247565; AAF65816.1; -
 CC EMBL: AF247789; AA958694.1; -
 CC EMBL: AF151048; AAF36134.1; ALT_FRAME.
 CC EMBL: BC000607; AAH00607.1; -
 CC Genew: HGNC:14452; ANAPC11.
 CC GK: Q9NMG5; -
 CC InterPro: IPR001841; Znf_ring.
 CC SMART: SMO0184; RING; 1.
 CC PROSITE: PS5089; 2F_RING_2; 1.
 CC Ubl conjugation pathway; Cell division; Mitosis; Zinc;
 CC Zinc-finger; Metal-binding; Nuclear protein; Ubl conjugation;
 CC Alternative splicing.
 CC ZN FING 34 77
 CC METAL 23 23
 CC METAL 26 26
 CC METAL 34 34
 CC METAL 37 37
 CC METAL 44 44
 CC METAL 51 51
 CC METAL 53 53
 CC METAL 56 56
 CC METAL 58 58
 CC METAL 59 59
 CC METAL 73 73
 CC METAL 76 76
 CC METAL 77 77
 CC VARSPLIC 1 37
 CC -----
 CC MUTAGEN 23 23
 CC C->S: GREATLY REDUCES AUTOUBIQUITINATION
 CC ACTIVITY.
 CC MUTAGEN 26 26
 CC C->S: GREATLY REDUCES AUTOUBIQUITINATION
 CC ACTIVITY.
 CC MUTAGEN 34 34
 CC C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
 CC ACTIVITY.
 CC MUTAGEN 37 37
 CC C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
 CC ACTIVITY.
 CC MUTAGEN 44 44
 CC C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
 CC ACTIVITY.
 CC MUTAGEN 51 51
 CC C->S: GREATLY REDUCES AUTOUBIQUITINATION
 CC ACTIVITY.
 CC MUTAGEN 53 53
 CC H->S: GREATLY REDUCES AUTOUBIQUITINATION

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 25, 2004, 09:17:20 / Search time 43 Seconds
(without alignments)
7455.035 Million cell updates/sec

Title: US-09-914-324a-3

Perfect score: 962
Sequence: 1 cccaaaatggcggcagcagat.....aaagtcacgttcgattctcg 508

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p_model -DB=us-09-914-324a-3 -UNAT 25032004 090847 8730/app query.fasta_1.647
-O=/cgm2/1/USPTO.spool.p/US09914324 -UNAT 25032004 090847 8730/app query.fasta_1.647
-DB=SPRMBL_25 -CPMT=fastan -SUFFIX=rspr -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blonuma62 -TRANS=human40.cai -LIST=45
-DOCLLEN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09914324 @CGN 1.1 86 @unat 25032004 090847 8730 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_protist.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvtnus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523.5	54.4	114	Q8S3S0	Oryza sativa

2	523	54.4	110	10	Q7Y042	Oryza sativa
3	416	43.2	122	11	Q9D105	Oryza sativa
4	378	39.3	107	10	Q7Y042	Oryza sativa
5	314.5	32.7	97	10	Q9FTN1	Oryza sativa
6	308	32.0	92	5	Q8SMU6	Oryza sativa
7	284.5	29.6	113	5	Q9V607	Oryza sativa
8	266	27.7	112	5	P91404	Oryza sativa
9	210	21.8	84	10	Q940X6	Oryza sativa
10	198	20.6	84	10	Q8J306	Oryza sativa
11	197	20.5	85	5	Q9V1J5	Oryza sativa
12	151	15.7	89	5	Q8IC08	Oryza sativa
13	146.5	15.2	135	5	Q20052	Oryza sativa
14	141	14.7	57	10	Q9M9L0	Oryza sativa
15	136	14.1	165	3	Q12157	Oryza sativa
16	132.5	13.8	99	10	Q9AVZ5	Oryza sativa
17	129.5	13.5	94	3	Q862L9	Oryza sativa
18	120.5	13.1	129	3	Q08272	Oryza sativa
19	116.5	12.1	2160	5	Q17709	Oryza sativa
20	112.5	11.7	911	3	Q96UD5	Oryza sativa
21	106.5	11.1	189	10	Q94J02	Oryza sativa
22	106	11.0	445	12	Q8KX10	Oryza sativa
23	105	10.9	349	10	Q9SU06	Oryza sativa
24	104	10.8	693	5	Q8A1U7	Oryza sativa
25	102.5	10.7	249	10	Q9C455	Oryza sativa
26	102.5	10.6	383	10	Q7X1Y9	Oryza sativa
27	102	10.6	151	10	Q9F1S5	Oryza sativa
28	102	10.6	210	10	Q9SD55	Oryza sativa
29	100	10.4	147	10	Q91JY5	Oryza sativa
30	100	10.4	650	10	Q84M33	Oryza sativa
31	100	10.3	676	10	Q9M1S2	Oryza sativa
32	99.5	10.3	207	5	Q7Y1Y5	Oryza sativa
33	99	10.3	524	10	Q815X8	Oryza sativa
34	99	10.3	494	10	Q9M1L1	Oryza sativa
35	98.5	10.2	571	3	Q94400	Oryza sativa
36	98	10.2	147	10	Q84M11	Oryza sativa
37	98	10.2	158	10	Q9SPM0	Oryza sativa
38	97.5	10.1	272	10	Q9F1A1	Oryza sativa
39	97.5	10.1	295	10	Q8H740	Oryza sativa
40	97.5	10.1	327	10	Q9C711	Oryza sativa
41	97.5	10.1	445	5	Q81D18	Oryza sativa
42	97	10.1	159	10	Q9L2V8	Oryza sativa
43	96.5	10.0	200	10	Q9ZT49	Oryza sativa
44	96.5	10.0	332	10	Q910M2	Oryza sativa
45	95.5	9.9	233	10	Q9F8Z7	Oryza sativa

ALIGNMENTS

RESULT 1
ID Q8S3S0 PRELIMINARY; PRT; 114 AA.
AC Q8S3S0;
DT 01-JUN-2002 (TREMBL) 21, Created
DT 01-JUN-2002 (TREMBL) 21, Last sequence update
DT 01-JUN-2003 (TREMBL) 24, Last annotation update
DE Putative ring box-1 protein.
GN 49P11.12.
OS Oryza sativa (japonica cultivar group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
CX NCBI_TaxID=3947;
RN (1)
RP STRAIN=CV. Nipponbare;
RC Park Y.-U., Roostoks N., Ramakrishna W., Samiguel P., Shiloff B.,
RA Ma J., Jiang Z., Kleinhofs A., Bennetzen J.;
RT "Sequence characterization of orthologous regions in the barley and rice genomes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF180496; AAL87158.1; -;
DR Gramene; Q8S3S0; -;
DR InterPro; IPR001841; ZnF_ring.

Db 1 MetAlaAlaMetAspValAspThrPro-AlaAlaProThrAlaAlaArgAlaAspSe 20
 QY 67 CGCTTTGAAGTGAAGAAAGTGAATGACAGTACCCCTCGGCGCTGAGTATTTGTTGAT 125
 Db 20 TAlaLeuLeuLeuLeuSerGlyMetGlnTrpProSerGlyArgGlyThrLeuTrpLeu1 40
 QY 127 AACTGTGCGCATCTCGAGAACCAACATTATGATCTTTGCATGAGATGTCAAGCTAACCGAG 186
 Db 40 eThrValProSerAlaGlyThrThrLeuTrpIlePheValSerAsnValArgProThrAr 60
 QY 187 GCGTCCGCTACTTTCAGAGAGTGTCTGCGATGGGAGTGTGTAACCATGCTTTTAC 246
 Db 60 gArgGlnLeuLeuProLysSerValArgLeuHisGlyIleuSerAlaThrMetLeuPhe1 80
 QY 247 TTCACATGATCTCTCGCTGCTGCTCAAAACAGACAGGTGTGTCCATTGGACACAGAGAG 306
 Db 80 eSerThrAlaSerLeuAspGlySerLysArgGlyArgGlyValArgTrpThrThrGluSe 100
 QY 307 TGGGAATTCCAAAAGTATGGGACACTAGGAAA 337
 Db 100 rGlySerSerArgSerMetGlyIleArgLys 110

RESULT 4

077367 PRELIMINARY: PRT: 107 AA.
 ID 077367
 AC 077367
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative ring finger protein.
 GN MAL3P6.28.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=35329;
 RX MEDLINE=99376085; PubMed=10448855;
 RP STRAIN=3D7;
 RC STRAIN=3D7;
 RA Bowman S., Lawson C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
 RA Churcher S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
 RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
 RA Horrocks P., Jagels R., Jassal B., Kyes S., McLean J., Mould S.,
 RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
 RA Rutter S., Skelton J., Squares R., Squares S., Sulten J.E.,
 RA Whitehead S., Woodward J.R., Newbold C., Barrett B.G.;
 RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
 falciparum .";
 RL Nature 400:532-538(1999).
 DR EMBL; Z98551; CAB1123.3; -.
 DR PIR; T18513; T18513.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4.1.
 DR SMART; SMC0184; RING.1.
 DR PROSITE; PSS0089; ZF_RING.2; 1.
 DR DR PROSITE; PSS0089; ZF_RING.2; 1.
 SQ SEQUENCE 107 AA; 12419 MW; C563432A60F20262 CRC64;

Alignment Scores:

Pred. No.: 4.2e-35 Length: 107
 Score: 378.00 Matches: 64
 Percent Similarity: 75.00% Conservative: 5
 Best Local Similarity: 69.57% Mismatches: 15
 Query Match: 39.29% Indels: 8
 Gaps: 1

US-09-914-324A-3 (1-508) x 077367 (1-107)

QY 70 TTGAGAGTGAAGAAAGTGAATGACAGTACCCCTCGGCGCTGAGTATTTGTTGATTAAC 129
 Db 13 PheYalLeuHisLysTrpSerAlaValAlaAlaTrpSerTrpAspIleSerValAspAsn 32
 QY 130 TGTGCGATCTGAGGAACCACTTATGATCTTTGCATGAGATGTCAAGCT----- 180

Db 33 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaLysThrThr 52
 QY 181 -----AACGAGCGCTCCCTACTTTCAGAAAGTGTACTGTGCGAGGGGA 225
 Db 53 AspHisGluAsnAspLysAspLysLysIleAspLysGluGlyCysThrValAlaTrpGly 72
 QY 226 GTCTGTAACTGATCTTTTCACTTCCACTGATCTCTCGCTGCGCTCAAAACAGACAGGTG 285
 Db 73 ValCysAsnHisAlaPheHisLeuHisCysIleSerArgTrpIleLysAlaArgGlnVal 92
 QY 286 TGTTCATTGGACACACAGAGAGTGGGAAATTCCAAAG 321
 Db 93 CysProLeuAspAsnThrThrTrpGluPheGlnLys 104

RESULT 5

09FTN1 PRELIMINARY: PRT: 97 AA.
 ID 09FTN1
 AC 09FTN1
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE P0005A05.18 protein (P0482C06.1 protein).
 GN P0005A05.18 OR P0482C06.1.
 OS Oryza sativa (rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzae; Oryza.
 NC NCB1_TaxID=4530;
 RX MEDLINE=99376085; PubMed=10448855;
 RP STRAIN=CV.
 RC STRAIN=CV.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0005A05.1";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0005A05.1";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP002865; BAB78605.1; -.
 DR Gramineae; Oryzae; Oryza.
 SQ SEQUENCE 97 AA; 10329 MW; FDD1CE7B5EDBA579 CRC64;

Alignment Scores:

Pred. No.: 1.09e-27 Length: 97
 Score: 314.50 Matches: 59
 Percent Similarity: 75.29% Conservative: 5
 Best Local Similarity: 69.41% Mismatches: 4
 Query Match: 32.69% Indels: 17
 Gaps: 2

US-09-914-324A-3 (1-508) x 09FTN1 (1-97)

QY 22 GATGTGATACCCCG-----AACGCGACCCAC 48
 Db 4 AspIleAsnAlaProProProProAlaProAlaProAlaGlyGluGlySerSer 23
 QY 49 AGCGCGCGGCG-----AAGAGCGCTTTGAAAGTGAAGTGAAT 90
 Db 24 SerAlaIleGlyProSerSerArgLysPheAsnLysArgPheGluIleLysLysTrpAsn 43
 QY 91 GCAGTAGCCCTCTGCGCTGAGATGTTGTTGATTAAGTGTGCGATCTGAGGAACAC 150
 Db 44 AlaValAlaLeuTrpAlaTrpAspIleValAlaAspAsnCysAlaIleCysArgAsnHis 63
 QY 151 ATTATGATCTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 210
 Db 64 IleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCys 83

RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Beran B., Carlson J.W., Celniker S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield B.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of Drosophila melanogaster genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dreanek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munoz J., Paclob U., Paragas V., Park S.,
 RA Patel S., Phouenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.,
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AEO03825; AAF58633.2; -;
 DR EMBL; AY113544; AAM29549.1; -;
 DR FLYBase; FBgn003641; CG8998.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 113 AA; 13101 MW; 41F16639A2EC1252 CRC64;

Alignment Scores:

Pred. No.: 3,58e-24 Length: 113
 Score: 284.50 Matches: 48
 Percent Similarity: 63.46% Conservative: 18
 Best Local Similarity: 46.15% Mismatches: 35
 Query Match: 29.57% Indels: 3
 DB: Gaps: 2

US-09-914-324a-3 (1-508) x Q9V607 (1-113)

QY 25 GTGATATCCCGGCGCGCACCC--AACAGCGCGCGGCAAGAGCGCTTGAATGAA 81
 Db 9 ValAspArgProThrAspAspGlyAspAlaGlyLysProGlnLysMetPheTrpLeuLys 28
 QY 82 AAGTGAATGACAGTACGCTCTGCGGCTGGAATATTTGGTGAATACATGTCATCTGC 141
 Db 29 LysTrpAsnAlaValAlaMetTrpSerTrpAspValGlnLysAspIleCysAlaIleCys 48
 QY 142 AGGAACACATATGATCTTTGATAGATGTCAGCTAACCAAGAGCGTCCGCTACT--- 198
 Db 49 ArgValGlnValMetAspSerCysLeuArgCysGlnAlaAspAsnLysArgAspValMet 68
 QY 199 ---TCAGAGAGTGTACTGTGCGCATGGGAGTCTGTATACCATGCTTTCACTTCAG 255
 Db 69 GLYArgGlnAspCysValAlaValTrpGlyGlnCysAsnHisSerPheHisLysCys 88
 QY 256 ATCTCTGCGTGCCTCAAAACACACAGAGTGTGTCATGACACAGAGAGTGGCAATTC 315
 Db 89 MetSerLeuTrpValLysGlnAsnAsnArgCysProLeuGlnGlnGlnTrpSerIle 108
 QY 316 CAAAGTATGAG 327
 Db 109 GlnArgMetGly 112

RESULT 8

P91404 PRELIMINARY; PRT; 112 AA.
 ID P91404
 AC P91404;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE R10A10.2 protein.
 GN R10A10.2
 OS Caenorhabditis elegans
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., De Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kireten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Smailson N., Smith A., Sornhamer E., Staden R., Sulston J.,
 RA Threlkery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Woldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wamsley, P., Bradshaw H.,
 RT "The sequence of C. elegans cosmid R10A10."
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterson R.,
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U80449; AB037826.1; -;
 DR PIR; T29620; T29620.
 DR HSSP; P28990; 1CHC.
 DR WormPep; R10A10.2; CE12670.
 DR InterPro; IPR001526; IY6 UPAR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SMO0184; RING; 1.
 DR PROSITE; PS50083; IY6 UPAR; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 112 AA; 12871 MW; 8F797E10FB701092 CRC64;

Alignment Scores:

Pred. No.: 5.2e-22 Length: 112
 Score: 266.00 Matches: 45
 Percent Similarity: 59.63% Conservative: 20
 Best Local Similarity: 41.28% Mismatches: 32
 Query Match: 27.65% Indels: 12
 DB: Gaps: 2

US-09-914-324a-3 (1-508) x P91404 (1-112)

QY 7 ATGGCGGAGAGATGATGATGATATACCCGAGCGGACCAACAGCGGCGGCGGAGAG 66
 Db 1 MetAsnAsnSerSerAsnAlaAspSerGlnGlnGlnSerThrSerAlaGlnLysGlnLys 20
 QY 67 CGC-----TTGAAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 102
 Db 21 ThrAlaAsnProSerGlnSerArgProPheValLeuLysLysTrpPheAlaLeuAlaVal 40
 QY 103 TGGCGCTGAGATATTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 162
 Db 41 TrpAlaTrpAspValGlnCysAspPheCysAlaIleCysArgValHisLeuMetGlnLys 60
 QY 163 TGCATAGATGATCAAGCTAACCAAGCGCTCCGCTACTTATGAGAAGTGTGATGATGATG 222

Dd	CysLeuArgCysGln-----SerGIuProserAlaGluCysTyrValValTrp	76
Qy	223 GGAGTCGTGAACCAAGCTTTTCACTCCATCGCATCTCTGGCGGCACAAACAGCACAG	282
Dd	77 GlyAspCysAAsHisSerPheIleHicScYcSmetThrGInTrpIleRgGlnAseAn	96
Qy	283 GTGTGTCTCATTTGGACAACAAGACAGTG	309
Dd	97 ArgCysProLeuCysGlnLysAspTrp	105
 RESULT 9 Q940X6 PRELIMINARY; PRT; 84 AA.		
ID	Q940X6;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE	Anaphase promoting complex subunit 11.	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophytia; Magnoliophytia; eudicotyledons; core eudicots; rosids;	
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsits.	
OX	NBI_TaxID=3702;	
RA	[1]	
RN	SEQUENCE FROM N.A.	
RP	Oktres L;	
RL	Submitted (JUG-2001) to the EMBL/Genbank/DDNJ databases.	
CC	-1-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	
DR	EMBL; AY052402; XAL13436.1; -	
DR	InetEprc; IPR001841; ZnF_Ling.	
DR	Pfam; PF00097; zF-C3HC4; 1.	
DR	SMART; SMO0184; RING; 1.	
KM	PROSITE; PSS0089; ZE_RING_2; 1.	
SC	Metal-binding; Zinc; Zinc-finger. SEQUENCE 84 AA; 9766 MW; Q49578FED95882D6 CRC64;	
 Alignment Scores: Pred. No.: 1.75e-15 Length: 84 Score: 210.00 Matches: 34 Percent Similarity: 59.09% Conservative: 18 Best local Similarity: 38.64% Mismatches: 28 Query Match: 21.83% Indels: 8 DB: Gaps: 3		
US-09-914-324A-3 (1-508) x Q940X6 (1-84) 		
Qy	67 CGCTTTGAAGTGAATAAGTAGAATGCCCTCTGGCGCTGGCATATTGTGTTGAT	126
Dd	2 LysValLysIleLeuYrgrPrHAIsAlaValAIasertPrThTPPSAlAGlnAspGl	21
Qy	127 AACGTGTCGCATTCGACAGAACCACATTAGATCTTTGGCATGAATGTCAACTAACAG	186
Dd	22 ThrcyselyleCysarGMetAlalpheArBGLYCysProASP CysLys-----	38
Qy	187 GCATCCCGCTACTTCAGAGAAGGTGTACTGTGCATGGGAGTGTGAACATGCTTTAC	244
Dd	39 -----LeuproglLysAspCysProLeuilelPrpGLYAICysAshisAlphenis	56
Qy	247 TTCACATGCATCTCTCGCTGGCTC-----AAAACAGACAGGTG---TGTCCATTGAC	297
Dd	57 LeuhiscylleleuYstrPrvalAanSenGInlTrserGlnAlahicCysproMetCys	76
Qy	298 AACAAGAGTGGGAATTCCAAAG	321
Dd	77 ArGaRGslutPrpGlnPhelySLu	84
 RESULT 10 O8H306 PRELIMINARY; PRT; 84 AA.		
ID	O8H306;	
DT	01-MAR-2003 (TREMBLrel. 23, Created)	
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	

DE Putative anaphase promoting complex subunit 11.
GN P0710F09.24.
OS Oryza sativa (Japanese cultivar-group).
OC Burkayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RL submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005325; BAC21540.1; -
DR Interpro: IPR001841; Znf ring.
DR Pfam: PF00097; zf-C3HC4_1.
DR PROSITE, PS50089; ZF_RING_2; 1
SQ SEQUENCE 84 AA; 9676 MW; 5CF99B1E32D5E09A CRC64;

Alignment Scores:
Pred. No.: 4.41e-14 Length: 84
Score: 198.00 Matches: 30
Percent Similarity: 57.47% Conservative: 20
Best Local Similarity: 34.48% Mismatches: 29
Query Match: 20.58% Indels: 8
DB: Gaps: 2

US-09-914-324A-3 (1-508) x Q8H306 (1-84)

QY 67 CGCTTGAAGTAAAGTGAATGCAAGAGCCCTCTGGGCGTGGATATTGGTTGAT 126
DB 2 Lyyvaalyslieuuglntrphisclyalaaeserrtrtrpaanaalaglnasglu 21
QY 127 AACTGTGCCATCTGCAGGAACCACTTATGATCTTTGCATGATGTCAGCTAACG 186
DB 22 Thrcygslyllecysarwmetralahaeaspglycyscysproaspcyslys----- 38
QY 187 GCGTCCGCTACTTCAGAGAAGGTACTGTGGCATGGGAGAGTCTGAACATGCTTTTCAC 246
DB 39 -----Pheproglyaspsapscysproleuiletrpglysercysasnhiialaphhis 56
QY 247 TTCACATGCATCTCTGCTGCTGCTCAAAACAG-----CAGGTGTGTTCATTGAC 297
DB 57 Leuhisegylleuulysrtrypalansersglntrsertrhproleucysprometcys 76
QY 298 AACGAGAGTGGGATTCGA 318
DB 77 ArgArgglutrlpelnphhis 83

RESULT 11
QYVLUS PRELIMINARY; PRT; 85 AA.
ID QYVLUS; Q8UL14;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG18042 protein (Putative ApC11 anaphase-promoting complex
DE subunit).
GN IMG ORF:CG18042.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA MEDLINE=2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gockyne J.D.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,


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QY 76 GTGAAAGAGTAGAGTAGAGCCCTGGCTGG---GATATTGGTTGATATAC--- 129
Db 6 VallylsArg11eH1sAlaValAlaArg17pLys1rIleGlySerThrIleAspSerVal 25
QY 130 TGTGCATCTGCGAGGACCAACATTATGATCTTTCATAGATGATCAAGCTAACCGAGG 189
Db 26 CysAlaIleCysAsnSerSerLeuGluAsnThrCysThrThrCysMet----- 41
QY 190 TCCGCTCTTCAGAGAGTAGTAGCTGCTGAGGAGTCTGATACCATGCTTTTCACTTC 249
Db 42 ---ArgProGlyAsnGlyCysProProlaPheIlylCysGlyHisIshisPheIshleu 60
QY 250 CACTGCATCTCTCGCTGCTGCTCAAAACACGACAGTG---TGTCCATTGACACACAGAGAG 306
Db 61 HisCysMetGluIlyStrIleIlyGlnAsnIlyshleuThrCysPProCysCysArgAlaAsp 80
QY 307 TGGGAATTCCAA 318
Db 81 TrpIlyrTyrglu 84

RESULT 13
Q20052 PRELIMINARY; PRT; 135 AA.
AC Q20052;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F35G12.9 protein.
GN F35G12.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditioidea;
OC Rhabditidae; Pelodetinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Chui C.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=99069613; PubMed=9851916;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RT Science 282:2012-2018(1998).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; Z46242; CA86328.1; -.
DR PIR; T21802; T21802.
DR WormPep; F35G12.9; CE00978.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 135 AA; 15512 MW; 1CC8BAF1AB67157 CRC64;

Alignment Scores:
Pred. No.: 4.94e-08 Length: 135
Score: 146.50 Matches: 28
Percent Similarity: 45.24% Conservative: 10
Best Local Similarity: 33.33% Mismatches: 35
Query Match: 15.23% Indels: 11
Gaps: 3

US-09-914-324A-3 (1-508) x Q20052 (1-135)
QY 76 GTGAAAGAGTAGAGTAGAGCCCTGGCTGG---GATATTGGTTGATATACGT 132
Db 53 VallylsArg11eH1sAlaValAlaArg17pLys1rIleGlySerThrIleAspSerVal 72
QY 133 GCCATCTGCGAGGACCAACATTATGATCTTTCATAGATGATCAAGCTAACCGAGGCTCC 192
Db 73 GlyIleCysArgMetGluPheGluSerAlaCys-----AsnMetCysIlys 87

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QY 193 GCTACTTCAGAGAGTAGTAGCTGCTGAGGAGTCTGTAAACGATCTTTCACCTTCAC 252
Db 88 PheProGlyAspArgCysProLeuValIleuGlyIleCysArgHisAlaPheHisArgHis 107
QY 223 TGCATCTCGCTGGCTC-----AAACACGACAGCTGTGTCCATTGGAC 297
Db 108 CysIleAspIlyStrIleAlaIleProThrAsnGlnProArgAlaGlnCysProLeuCys 127
QY 298 AACAGAGAGTG 309
Db 128 ArgGlnAspTrp 131

RESULT 14
Q9M9L0 PRELIMINARY; PRT; 57 AA.
ID Q9M9L0;
AC Q9M9L0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F10A16.17 protein.
GN F10A16.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidops.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Roming C.M., Koo H., Fujii C.Y., Utechtack T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL "Arabidopsis thaliana chromosome III BAC F10A16 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC EMBL; AC012393; AAF26089.1; -.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 57 AA; 6580 MW; 504C753B7B745C74 CRC64;

Alignment Scores:
Pred. No.: 1.91e-07 Length: 57
Score: 141.00 Matches: 23
Percent Similarity: 62.50% Conservative: 12
Best Local Similarity: 41.07% Mismatches: 13
Query Match: 14.66% Indels: 8
Gaps: 3

US-09-914-324A-3 (1-508) x Q9M9L0 (1-57)
QY 163 TGCATGAGTAGAGTAGAGCTGAGGAGTCTGTAAACGATCTTTCACCTTCAG 222
Db 7 CysProAspCysIlyS-----LeuProGlyAspArgCysProLeuIleTrp 21
QY 223 GGAGTGTGAACCATGCTTTTCATCTCCATGATCTCTCGTGGCTC-----AAACA 276
Db 22 GlyAlaCysAsnHisAlaPheHisIleuHisCysIleLeuIlyStrIlyValAsnSerGlnThr 41
QY 277 CCAGAGAGTG---TGTCCATTGAGACACAGAGAGTGGGAATTCACAAAG 321
Db 42 SerGlnAlaHisCysProMetCysArgArgGluTrpGlnPheIlyGlu 57

RESULT 15
Q12157 PRELIMINARY; PRT; 165 AA.
ID Q12157;
AC Q12157;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chromosome IV reading frame ORF YDL008W.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:32:07 ; Search time 21 seconds
(without alignments)

494.699 Million cell updates/sec

Title: US-09-914-324A-1

Sequence: 1 MAAMDVDTPTSGTNSGAKK.....KTROYCPLDNREMEFQKXGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96151526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: Tr1: *
2: Tr2: *
3: Tr3: *
4: Tr4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	108	2	T51146 ring-box protein 1
2	510	82.8	136	2	T13388 hypothetical prote
3	439	81.0	115	2	T47341 ring-box protein-1
4	433	80.0	110	2	T27823 hypothetical prote
5	469	76.1	107	2	T38310 pop-interacting pr
6	385	62.5	121	2	S66830 hypothetical prote
7	378	61.4	166	2	T18513 hypothetical prote
8	266	43.2	112	2	T29620 hypothetical prote
9	164.5	26.7	94	2	T36652 hypothetical prote
10	146.5	23.8	135	2	T21802 hypothetical prote
11	136	22.1	165	2	S52511 hypothetical prote
12	132.5	21.5	99	2	G90113 Rbp1 protein (lipo
13	116.5	18.9	2160	2	T20241 hypothetical prote
14	104	16.9	349	2	T06680 hypothetical prote
15	102.5	16.6	249	2	T45654 probable RING zinc
16	102	16.6	210	2	T45654 zinc-finger-like p
17	100	16.2	676	2	T47637 hypothetical prote
18	97	15.7	159	2	T48209 hypothetical prote
19	97	15.7	327	2	D86474 probable RING zinc
20	96	15.6	332	2	D86448 hypothetical prote
21	95.5	15.5	441	2	F71425 hypothetical prote
22	95	15.4	253	2	T06113 hypothetical prote
23	95	15.4	322	2	H85474 hypothetical prote
24	95	15.4	336	2	T28358 ORF MSY197 tyrosop
25	95	15.4	362	2	T51464 RING-H2 zinc finger
26	95	15.4	530	2	T50499 hypothetical prote
27	95	15.4	689	2	F84811 probable retroelem
28	92	14.9	185	2	T51844 RING-H2 finger pro
29	91.5	14.9	190	2	T51859 RING-H2 finger pro

30	91.5	14.9	496	2	B96674 hypothetical prote
31	91.5	14.9	571	2	T40911 probable PHD-type
32	91	14.8	530	2	T28366 ORF MSY205 tryptop
33	90.5	14.7	677	2	T39713 zinc finger protei
34	90	14.6	213	2	T14811 hypothetical prote
35	90	14.6	532	2	T49467 related to Cobl-in
36	90	14.6	1208	2	T05077 hypothetical prote
37	89.5	14.5	202	2	T06621 hypothetical prote
38	89.5	14.5	624	2	T01585 probable RING zinc
39	89	14.4	357	2	E85092 hypothetical prote
40	89	14.4	456	2	T19377 hypothetical prote
41	88.5	14.4	336	2	A86406 probable RING zinc
42	88.5	14.4	524	2	F96572 protein F12M5.10
43	88	14.3	515	2	S15788 intermediate early
44	88	14.3	161	2	E88541 protein ZK637.14
45	88	14.3	200	2	T41745 RING-H2 finger pro

ALIGNMENTS

RESULT 1
T51146
ring-box protein 1 [imported] - human
C:Species: Homo sapiens (man)
C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C:Accession: T51146
R:Kamura, T., Keop, D.M., Conrad, M.N., Skowrya, D., Moreland, R.J., Illopoulos, O., Le
Science 284, 657-661, 1999
A:Title: Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase.
A:Reference number: 225317, PMID:9234320, PMID:10213691
A:Accession: T51146
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-108 <KAM>
A:Cross-references: EMBL:AF140598; PIDN:AA029715.1
C:Genetics:
A:Gene: RBX1

Query Match 100.0%; Score 616; DB 2; Length 108;
Best local similarity 100.0%; Pred.No.1.5e-58;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MAAMDVDTPTSGTNSGAKKFEVKKNAVALAMADIIVDNCAICRNHIMDICEQANG 60
Db 1 MAAMDVDTPTSGTNSGAKKFEVKKNAVALAMADIIVDNCAICRNHIMDICEQANG 60
Cy 61 ASATSECTVAMGVCNHAFFHCISRWLKTROYCPLDNREMEFQKXGH 108
Db 61 ASATSECTVAMGVCNHAFFHCISRWLKTROYCPLDNREMEFQKXGH 108

RESULT 2

T13388
hypothetical protein 115C2.11 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13388
R:Salles, C., Valenti, P., Darlamitso, A., Henderson, N., Campbell, L., Glover, D.
submitted to the EMBL data library, May 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: 21765
A:Accession: T13388
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-136 <CAT>
A:Cross-references: EMBL:AL031581; PIDN:CAA20888.1
C:Genetics:
A:Cross-references: Flybase:FBgn0020381
A:Introns: 64/7
A>Note: EG:115C2.11
Query Match 82.8%; Score 510; DB 2; Length 136;

A:Cross-references: SGD:S0005493
 A:Map position: 15L
 A>Note: YOL133w
 C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match 62.5%; Score 385; DB 2; Length 121;
 Best Local Similarity 56.6%; Pred. No. 6, 9e-34;
 Matches 64; Conservative 10; Mismatches 29; Indels 10; Gaps 1;

5 MDVDTPTSGTNSGAG-----KKRPVKKNNAVALMAMDIVVNDCAICRNHIMDL 54
 Db 8 MDVDEDSQNIASSNQSAPEVETKKRFEIKKMTAVAFMSWDIAVDNCAICRNHIMBPI 67

QY 55 ECGANASATSECTVANGVCNNAHFPHICISRMKTRQVCPIDNREMEFQKG 107
 Db 68 ECGPKMTDITNECVAMAGVCNNAHFPHICINIKTRKDCPLDNQPMQLARCG 120

RESULT 7
 T18513
 hypothetical protein C0845c - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T18513

R:Lawson, D.; Bowman, S.; Barrell, B.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z18935

A:Accession: T18513
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-166 <LAW>
 A:Cross-references: EMBL:Z98551; PIDN:CAB1123.2

C:Genetics:
 A:Map position: 3
 A:introns: 19/1
 A>Note: C0845c

Query Match 61.4%; Score 378; DB 2; Length 166;
 Best Local Similarity 59.6%; Pred. No. 5, 2e-33;
 Matches 64; Conservative 5; Mismatches 15; Indels 8; Gaps 1;

QY 22 FEVKNNNAVALMAMDIVVNDCAICRNHIMDLCEGCA-----NQASATSECTVANG 73
 Db 72 FKHKMSAVAMWMDISVNDCAICRNHIMDLCEGCAKTTDENDKRIKREGCTVANG 131

QY 74 VCNNAHFPHICISRMKTRQVCPIDNREMEFQK 105
 Db 132 VCNNAHFPHICISRMKTRQVCPIDNREMEFQK 163

RESULT 8
 T29620
 hypothetical protein R10A10.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002

R:Wamsley, P.; Bradshaw, H.
 submitted to the EMBL Data Library, November 1996

A:Description: The sequence of C. elegans cosmid R10A10.
 A:Reference number: Z20653

A:Accession: T29620
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-112 <WAM>

A:Cross-references: EMBL:U60449; PIDN:AAB37826.1; GSPDB:GN00019; CESP:R10A10.2
 A:Experimental source: strain Bristol N2; clone R10A10

C:Genetics:
 A:Gene: CESP:R10A10.2

A:Map position: 1
 A:introns: 17/2; 59/1

C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology
 Query Match 43.2%; Score 266; DB 2; Length 112;

Best Local Similarity 41.3%; Pred. No. 3e-21;
 Matches 45; Conservative 20; Mismatches 32; Indels 12; Gaps 2;

QY 1 MAAMDVDTPTSGTNSGAGKKR-----FEVKNNNAVALMAMDIVVNDCAICRNHIMDL 52
 Db 1 MNNSNVDSQEGSTAKQKRTANPSESPPFLVKNNNAVALMAMDIVVNDCAICRNHIMB 60

QY 53 CIECGANASATSECTVANGVCNNAHFPHICISRMKTRQVCPIDNREMEFQKG 101
 Db 61 CLRCQ-----SEPSAECTVANGDCNHSFHHCKMTQWIRKNNRCPFLCQKDW 105

RESULT 9
 T38652
 hypothetical protein SPAC343.03 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38652

R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21804

A:Accession: T38652
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-94 <MDR>

A:Cross-references: EMBL:AL109739; NID:e1534774; PIDN:CAB52266.1; GSPDB:GN00066; SPDB:SI

A:Experimental source: strain 972h-; cosmid c343
 C:Genetics:
 A:Gene: SPDB:SPAC343.03
 A:Map position: 1
 A:introns: 7/1; 48/1

Query Match 26.7%; Score 164.5; DB 2; Length 94;
 Best Local Similarity 33.7%; Pred. No. 1, 7e-10;
 Matches 28; Conservative 16; Mismatches 30; Indels 9; Gaps 3;

QY 21 FEVKNNNAVALMAMDIVVNDCAICRNHIMDLCEGCAQASATSECTVANGVCNNAHF 79
 Db 2 KVKILRYHAIAAMTWMDIPKDDVCGICRVPFGCCPQC-----TSPGDNCTVWGKCHIT 56

QY 80 HFHCISRMKLT---RQVCPIDNR 99
 Db 57 HAHCIQWMLATSSGSGGCPMDRQ 79

RESULT 10
 T21802
 hypothetical protein F35G12.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002

R:Chui, C.
 submitted to the EMBL Data Library, October 1994

A:Reference number: Z19473
 A:Accession: T21802

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-135 <WIL>

A:Cross-references: EMBL:Z46242; PIDN:CAA86328.1; GSPDB:GN00021; CESP:F35G12.9

A:Experimental source: clone F35G12
 C:Genetics:

A:Gene: CESP:F35G12.9
 A:Map position: 3

A:introns: 33/3; 57/3
 C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

F:68-133/Domain: RING finger homology <RXN>

Query Match 23.8%; Score 146.5; DB 2; Length 135;
 Best Local Similarity 33.3%; Pred. No. 2e-08;
 Matches 28; Conservative 10; Mismatches 35; Indels 11; Gaps 3;

QY 24 VKKNNAVALMAM-DIVVNDCAICRNHIMDLCEGCAQASATSECTVANGVCNNAHFH 82

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:24:27 ; Search time 55 Seconds
(without alignments)
554.821 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMDVDPISGTSGAGKK.....KTRGVCPIDNREWFQYXGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp19806:*
2: geneseqp19806:*
3: geneseqp20008:*
4: geneseqp20008:*
5: geneseqp20025:*
6: geneseqp20035:*
7: geneseqp20035:*
8: geneseqp20045:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	108	3 AAB19160	AAB19160 Amino aci
2	616	100.0	108	3 AAB08813	AAB08813 A human c
3	616	100.0	108	3 AAG03890	AAG03890 Human sec
4	616	100.0	108	4 AAB47559	AAB47559 ROC1. 1/2
5	616	100.0	108	4 AAB47559	AAB47559 Human RIN
6	616	100.0	108	4 ADC02481	ADC02481 RING fing
7	534	86.7	108	4 ABB68080	ABB68080 Drosophil
8	514.5	83.5	108	3 AAG23004	AAG23004 Arabidops
9	511	83.0	109	3 AAG23005	AAG23005 Arabidops
10	400.5	65.0	122	4 ABB66109	ABB66109 Drosophil
11	385	62.5	121	3 AAB08814	AAB08814 A yeast c
12	383	52.4	57	3 AAB41007	AAB41007 Human ORF
13	292	47.4	113	3 AAY06492	AAY06492 Human sen
14	292	47.4	113	3 AAB43295	AAB43295 Human ORF
15	292	47.4	118	4 AAU15873	AAU15873 Human nov
16	292	47.4	118	6 AAB05942	AAB05942 Human nov
17	292	47.4	131	4 AAU16332	AAU16332 Human nov
18	292	47.4	131	6 AAB055401	AAB055401 Human nov
19	291	47.2	113	2 AAY06509	AAY06509 Human sen
20	290.5	47.2	113	2 AAY06491	AAY06491 Mouse sen
21	290.5	47.2	113	2 AAB19161	AAB19161 Amino aci
22	287	46.6	113	4 AAB47600	AAB47600 ROC2. 1/2
23	287	46.6	113	5 AAB24621	AAB24621 Human RIN
24	287	46.6	113	7 ADC02483	ADC02483 RING fing
25	285	46.3	113	2 AAY06506	AAY06506 Human sen

26	283	45.9	113	2 AAY06500	AAY06500 Human sen
27	283	45.9	113	2 AAY06501	AAY06501 Human sen
28	282	45.8	113	2 AAY06496	AAY06496 Human sen
29	282	45.8	113	2 AAY06503	AAY06503 Human sen
30	282	45.8	113	2 AAY06502	AAY06502 Human sen
31	282	45.8	113	2 AAY06506	AAY06506 Human sen
32	282	45.8	113	2 AAY06495	AAY06495 Human sen
33	282	45.8	113	2 AAY06499	AAY06499 Human sen
34	282	45.8	113	2 AAY06498	AAY06498 Human sen
35	282	45.8	113	2 AAY06505	AAY06505 Human sen
36	274	44.5	113	2 AAY06504	AAY06504 Human sen
37	272	44.2	113	2 AAY06497	AAY06497 Human sen
38	272	44.2	113	2 AAY06507	AAY06507 Human sen
39	235	38.1	97	2 AAY06494	AAY06494 Human sen
40	235	38.1	97	3 AAB43284	AAB43284 Human ORF
41	213	34.6	86	3 AAB58912	AAB58912 Breast an
42	213	34.6	88	4 ABB12308	ABB12308 Human HSP
43	213	34.6	88	4 AAB79609	AAB79609 Human pro
44	213	34.6	91	5 ABB41805	ABB41805 Human ova
45	213	34.6	105	4 AAU16321	AAU16321 Human nov

ALIGNMENTS

RESULT 1
AAB19160
ID AAB19160 standard; protein; 108 AA.
XX
AC AAB19160;
XX
DT 19-FEB-2001 (first entry)
XX
DE Amino acid sequence of human ring finger protein ROC1.
XX
KW ROC1; ROC2; cullin; ring finger protein; APC1; APC complex; SCF pathway;
KW cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
KW tumour.
XX
OS Homo sapiens.
XX
PN MO200058472-A2.
PD 05-OCT-2000.
PF 31-MAR-2000; 2000MO-US006592.
PR 31-MAR-1999; 99US-0127261P.
PR 22-NOV-1999; 99US-0166927P.
PA (UNNC-) UNIV NORTH CAROLINA.
PI Xiong Y, Ohta T;
XX WPI; 2000-647235/62.
DR N-PSDB; AAA96882.
XX
PT Novel nucleic acid encoding cullin regulating ring finger proteins,
PT termed as ROC proteins similar to anaphase-promoting complex 11, for
PT therapeutic and diagnostic use.
PS Claim 9; Fig 2A; 83pp; English.
XX
XX The present sequence represents a human ROC1 ring finger protein. The
XX specification also describes human ROC2. ROC1 and ROC2 are similar to
XX APC1, a subunit of the APC complex. The proteins stimulate cullin
XX dependent ubiquitin ligase activity. ROC1 functions in vivo as an
XX essential regulator of CDK inhibitor Sic1 degradation by the SCF
XX (undefined) pathway. ROC proteins are useful for screening bioactive
XX agents that interfere with the binding of ROC proteins with cullin
XX proteins. Pharmaceutical formulations comprising ROC proteins are useful
XX for diagnostic and therapeutic purposes, preferably for diagnosing and
XX treating tumours

XX Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIIVNCAICRHHIMDLCTECQANQ 60
1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIIVNCAICRHHIMDLCTECQANQ 60

DB 61 ASATSECTVAMGVCNNAFHFCISRMLKTRQVCPDLNREWEFQKYG 108
61 ASATSECTVAMGVCNNAFHFCISRMLKTRQVCPDLNREWEFQKYG 108

RESULT 2

AA08813 ID AAB08813 standard; protein; 108 AA.

XX AAB08813;

DT 02-JAN-2001 (first entry)

XX A human cullin-interacting RING-H2 finger protein (Rbx1).

XX Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
XX tumour suppressor; carcinoma; Ring box associated carcinoma;
XX von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
XX cerebellar hemangioblastoma; hemangioma; retinal angiomata;
XX pheochromocytomas.

XX Homo sapiens.

XX MO200050445-A1.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000MO-US004838.

XX 26-FEB-1999; 99US-0121787P.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX Conway JA, Conway RC, Kamura T;

XX WPI; 2000-572067/53.

XX N-PSDB; AAA74978.

XX Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and Skp1-Cdc53P-F-box protein (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box protein associated carcinomas.

XX Claim 1; Page 34; 37pp; English.

XX The present sequence represents a human cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The polypeptide is a tumour suppressor. Rbx1 is useful for diagnosing a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting metabolically deficient system in animals. Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Rbx1 can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau) complex controlling the conjugation of ubiquitin or ubiquitin-like proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal angiomata and pheochromocytomas

XX Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;

Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIIVNCAICRHHIMDLCTECQANQ 60
1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIIVNCAICRHHIMDLCTECQANQ 60

DB 61 ASATSECTVAMGVCNNAFHFCISRMLKTRQVCPDLNREWEFQKYG 108
61 ASATSECTVAMGVCNNAFHFCISRMLKTRQVCPDLNREWEFQKYG 108

RESULT 3

AA03890 ID AAG03890 standard; protein; 108 AA.

XX AAG03890;

DT 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 7971.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000/2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GSEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX N-PSDB; AAC03896.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 7971; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or poly(A)-RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors

XX Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIIVNCAICRHHIMDLCTECQANQ 60
1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIIVNCAICRHHIMDLCTECQANQ 60

DB 61 ASATSECTVAMGVCNNAFHFCISRMLKTRQVCPDLNREWEFQKYG 108
61 ASATSECTVAMGVCNNAFHFCISRMLKTRQVCPDLNREWEFQKYG 108

Db 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108

RESULT 4

AA847599 standard; protein; 108 AA.

AA847599;

07-JAN-2002 (first entry)

ROCI.

Assay; ubiquitin ligase; tag1-ubiquitin; E1, E2;
Kw ubiquitin activating enzyme; ubiquitin conjugating enzyme; E3;
Kw ubiquitin ligase; ubiquitination modulator.

Unidentified.

W0200175145-A2.

11-OCT-2001.

03-APR-2001; 2001WO-US010906.

03-APR-2000; 2000US-00542497.

(RIGE-) RIGEL PHARM INC.

Iseakani SD, Huang J, Sheung J, Pray TR;

WPI; 2001-626445/72.

Assaying ubiquitin ligase activity for identifying modulators of
ubiquitination, by combining ubiquitin, ubiquitin activating conjugating
enzyme, ubiquitin ligase and measuring amount of ubiquitin bound to the
ligase.

Example 1; Fig 11; 98pp; English.

The sequences given in AA847596-602 are proteins which may be used in the
method of the invention for assaying ubiquitin ligase activity. The
method comprises combining under conditions that favour ubiquitin ligase
activity, tag1-ubiquitin, E1 (ubiquitin activating enzyme), E2 (ubiquitin
conjugating enzyme) and E3 (ubiquitin ligase) and measuring the amount of
tag1-ubiquitin bound to the E3. The method is useful for assaying
ubiquitin ligase activity and ubiquitination enzyme activity which is
useful for identifying ubiquitination modulator. The method comprises
combining tag1-ubiquitin, the modulator, E1, E2 and tag2-E3 and measuring
the amount of tag1-ubiquitin bound to tag2-E3 or combining tag1-
ubiquitin, modulator, E1 and tag3-E2 and measuring the amount of tag1-
ubiquitin bound to tag3-E2. Ubiquitin ligase activity is measured
directly, eliminating the need for target proteins and subsequent
analysis such as separating ligated from unligated material in an SDS-
PAGE procedure. This allows multi-well array analysis and high throughput
screening techniques for modulators of ubiquitination activity. The
method also allows the analysis of many different combinations of E3
components and E2/E3 combinations without requiring prior identification
of specific target substrates. Ubiquitin is labeled, directly or
indirectly and this allows for easy and rapid detection and measurement
of ligated ubiquitin

Sequence 108 AA;

Query Match 100.0%; Score 616; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMVDPTSGTNSGAKGRFEVKKNAVALAMWDIVDNCALCRNHIMDLICIEQANQ 60
1 MAAMVDPTSGTNSGAKGRFEVKKNAVALAMWDIVDNCALCRNHIMDLICIEQANQ 60
Db

QY 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108
Db 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108

RESULT 5

AAE24620 standard; protein; 108 AA.

AAE24620;

22-OCT-2002 (first entry)

Human RING finger protein, ROCI.

Ubiquitin ligase; Ub; tag1-ubiquitin; E1; ubiquitin-activating enzyme;
Kw E2; ubiquitin-conjugating enzyme/ubiquitin carrier protein; E3; human;
Kw RING finger protein.

Homo sapiens.

US2002042083-A1.

11-APR-2002.

03-APR-2001; 2001US-00826312.

03-APR-2000; 2000US-00542497.

(RIGE-) RIGEL PHARM INC.

Iseakani SD, Huang J, Sheung J, Pray TR;

WPI; 2002-488718/52.

Assay for ubiquitin ligase activity, useful for identifying modulators,
by measuring binding of labeled ubiquitin to ubiquitin ligase.

Disclosure; Fig 11; 56pp; English.

The invention relates to an assay for ubiquitin ligase (UL) activity
which comprises incubating tag1-ubiquitin, E1 (ubiquitin-activating
enzyme), E2 (ubiquitin-conjugating enzyme/ubiquitin carrier protein) and
E3 (UL) and measuring the amount of tag1-ubiquitin bound to E3. The
method is particularly used to screen for modulators of UL activity. The
present sequence is human RING finger protein, ROCI

Sequence 108 AA;

Query Match 100.0%; Score 616; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMVDPTSGTNSGAKGRFEVKKNAVALAMWDIVDNCALCRNHIMDLICIEQANQ 60
1 MAAMVDPTSGTNSGAKGRFEVKKNAVALAMWDIVDNCALCRNHIMDLICIEQANQ 60
Db

QY 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108
61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108
Db

RESULT 6

ADC02481 standard; protein; 108 AA.

ADC02481;

18-DEC-2003 (first entry)

RING finger protein ROCI.

ubiquitin; Mdm2; p53; RING finger protein; ROCI.

PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 14-MAY-1999; 99US-0134768P.
PR 18-MAY-1999; 99US-0134941P.
PR 19-MAY-1999; 99US-0135124P.
PR 20-MAY-1999; 99US-0135353P.
PR 21-MAY-1999; 99US-0135629P.
PR 24-MAY-1999; 99US-0136021P.
PR 25-MAY-1999; 99US-0136392P.
PR 27-MAY-1999; 99US-0136782P.
PR 28-MAY-1999; 99US-0137222P.
PR 01-JUN-1999; 99US-0137528P.
PR 03-JUN-1999; 99US-0137502P.
PR 04-JUN-1999; 99US-0137724P.
PR 07-JUN-1999; 99US-0138094P.
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PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139112P.
PR 16-JUN-1999; 99US-0139453P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142820P.
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PR 15-JUL-1999; 99US-0144005P.
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PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145214P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145912P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147316P.
PR 06-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 20-AUG-1999; 99US-0149930P.
PR 22-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0150566P.
PR 25-AUG-1999; 99US-0150884P.
PR 26-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151388P.
PR 01-SEP-1999; 99US-0151930P.
PR 01-SEP-1999; 99US-0152633P.
PR 07-SEP-1999; 99US-0153070P.
PR 10-SEP-1999; 99US-0153758P.
PR 13-SEP-1999; 99US-0154018P.
PR 15-SEP-1999; 99US-0154039P.
PR 16-SEP-1999; 99US-0154779P.
PR 20-SEP-1999; 99US-0155139P.
PR 22-SEP-1999; 99US-0155486P.
PR 23-SEP-1999; 99US-0155659P.
PR 24-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 29-SEP-1999; 99US-0157117P.
PR 04-OCT-1999; 99US-0157753P.
PR 05-OCT-1999; 99US-0157865P.
PR 06-OCT-1999; 99US-0158029P.
PR 07-OCT-1999; 99US-0158212P.
PR 08-OCT-1999; 99US-0158369P.
PR 12-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159299P.
PR 14-OCT-1999; 99US-0159330P.

PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 25-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161932P.
PR 29-OCT-1999; 99US-0162142P.
Query Match 83.5%; Score 514.5; DB 3; Length 118;
Best Local Similarity 78.6%; Pred. No. 2,7e-52;
Matches 92; Conservative 6; Mismatches 8; Indels 11; Gaps 2;
QY 3 AAMDVDT---PSG-----TNSGAGKKKEFEVKNNNAVALMMDIVDNCALCRHMD 51
Db 2 ATLDDSDVTMPAGASSSVASSSNKKAKKFELEIKKMSAVLWMDIVDNCALCRHMD 61
QY 52 LCIECQANQASATSECTVAMGVGNFAHFHFCISRMILKTROVPLDNRKWEFOKXCH 108
62 LCIECQANQASATSECTVAMGVGNFAHFHFCISRMILKTROVPLDNRSEWEFOKXCH 118
RESULT 9
AAG23005
ID AAG23005 standard; protein; 109 AA.
XX AAG23005;
AC AAG23005;
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26149.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
PN EP1033405-A2.
XX 06-SEP-2000.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 01-APR-1999; 99US-0128234P.
PR 06-APR-1999; 99US-0128714P.
PR 08-APR-1999; 99US-0128845P.
PR 16-APR-1999; 99US-0130077P.
PR 19-APR-1999; 99US-0130449P.
PR 21-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136031P.
PR 25-MAY-1999; 99US-0136382P.
PR 27-MAY-1999; 99US-0136782P.
PR 28-MAY-1999; 99US-0137222P.
PR 01-JUN-1999; 99US-0137528P.
PR 03-JUN-1999; 99US-0137529P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139464P.
PR 18-JUN-1999; 99US-0139465P.
PR 18-JUN-1999; 99US-0139466P.
PR 18-JUN-1999; 99US-0139467P.
PR 18-JUN-1999; 99US-0139468P.
PR 22-JUN-1999; 99US-0139859P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140655P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140911P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 19-JUL-1999; 99US-0144336P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144633P.
PR 20-JUL-1999; 99US-0144884P.

PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145102P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145224P.
PR 23-JUL-1999; 99US-0145276P.
PR 26-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0146171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149366P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149923P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155132P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 24-SEP-1999; 99US-0156596P.
PR 29-SEP-1999; 99US-0156598P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.

PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 83.0%; Score 511; DB 3; Length 109;
Best Local Similarity 88.8%; Pred. No. 6, 3e-52;
Matches 87; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 11 SGTNSGAGKREVEKKNAVALMWDIVVNDCAICRNHIMDLCICRQANQASATSECTV 70

Db 12 AASSNKKAKRFELIKMSAVNALMWDIVVNDCAICRNHIMDLCICRQANQASATSECTV 71

QY 71 AMGVCHNAHFHCISRMKTRQVCPDLSNEMEFQKXGH 108

Db 72 AMGVCHNAHFHCISRMKTRQVCPDLSNEMEFQKXGH 109

RESULT 10

ABB66109 standard; protein; 122 AA.

AC ABB66109;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 25119.

KM Drosophila; developmental biology; cell signalling; insecticide;

pharmaceutical.

XX Drosophila melanogaster.

PN W0200171042-A2.

XX 27-SEP-2001.

PE 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0151637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL10212.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

PS interactions.

CC Disclosure; SEQ ID NO 25119; 21np + Sequence Listing; English.
CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB13011), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_poc_sequences

XX Sequence 122 AA;

Query Match 65.0%; Score 400.5; DB 4; Length 122;
 Best Local Similarity 65.4%; Pred. No. 6.7e-39;
 Matches 70; Conservative 13; Mismatches 19; Indels 5; Gaps 2;

OY 5 MDVDTSGTNSG-AGKKFEVKKNNAVAMWDIVVNCACRHHIMDLCECOANO 60
 DB 16 MDNDDEPSSGSGAVQARTERFVKKVMVAHAMGMVAVDNCAICRHHIMDLCECOAD- 74
 OY 61 ASATSECTVAMGVGNHAFHFCISRWLKTRVCPIDNREMEFQKYG 107
 DB 75 PNNODECTVAMGECNHAFFHFCIAFWLXTRVCPIDNREMEVYQKYG 121

RESULT 11

AB08814 standard; protein; 121 AA.

AC AAB08814;

DT 02-JAN-2001 (first entry)

DE A yeast cullin-interacting RING-H2 finger protein (Rbx1).

XX Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
 XX tumour suppressor; carcinoma; Ring box associated carcinoma;
 XX von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
 XX cerebellar hemangioblastoma; hemangioma; retinal angiomatosis;
 XX pheochromocytomas.

OS Saccharomyces cerevisiae.

PN W0200050445-A1.

PD 31-AUG-2000.

PF 25-FEB-2000; 2000WO-US004838.

PR 26-FEB-1999; 99US-0121787P.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA Conway JA, Conway RC, Kamura T;

XX WPI, 2000-572067/53.

DR N-PSDB; AAA74979.

XX Cullin interacting RING-H2 finger protein, a component of von Hippel-
 PT Lindau tumor suppressor complex and Skp1-Cdc53P-F-box protein (SCF)
 PT ubiquitin ligase, useful for diagnosing and treating Ring box protein
 PT associated carcinomas.

PS Disclosure, Page 34-35; 37pp; English.

XX The present sequence represents a yeast cullin-interacting RING-H2 finger
 CC protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide
 CC is a tumour suppressor. Human Rbx1 is useful for diagnosing a
 CC predisposition of a patient to certain carcinomas. It is also useful for
 CC treating Ring box protein associated carcinomas or augmenting
 CC metabolically deficient systems in animals. Human Rbx1 is also useful for
 CC evaluating the effectiveness of a therapeutic treatment for Ring box
 CC associated carcinomas. Human Rbx1 can be used to screen for agents which
 CC augment or inhibit the activity of other cullin-containing ubiquitin

CC ligase and of the VHL (von Hippel-Lindau) complex controlling the
 CC conjugation of ubiquitin or ubiquitin-like proteins to various sets of
 CC target proteins. Carcinomas which may be treated include renal
 CC carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal
 CC angiomatosis and pheochromocytomas

XX Sequence 121 AA;

Query Match 62.5%; Score 385; DB 3; Length 121;
 Best Local Similarity 56.6%; Pred. No. 4.4e-37;
 Matches 64; Conservative 10; Mismatches 29; Indels 10; Gaps 1;

OY 5 MDVDTSGTNSGAG-----KKRFEVKKNNAVAMWDIVVNCACRHHIMDLCEI 54
 DB 8 MDVDEDSQNIAGSSNOSAFVETKKRFEVKKNNAVAMWDIVVNCACRHHIMDLCEI 67
 OY 55 EQQANASATSECTVAMGVGNHAFHFCISRWLKTRVCPIDNREMEFQKYG 107
 DB 68 ECPKAMTDIDNECVAMGVGNHAFHFCISRWLKTRVCPIDNREMEFQKYG 120

RESULT 12

AB041007 standard; protein; 57 AA.

AC AAB41007;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF771 polypeptide sequence SEQ ID NO:1542.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 XX human; antiparasitic; antiparkinsonian; noctropic; neuroprotective;
 XX immunomodulant; osteoporolytic; antidiabetic; immunosuppressant; cardiac;
 XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 XX hypotensive; dermatological; immunosuppressive; antineoplastic;
 XX antiviral; antibacterial; antifungal; antineuritic; antitumor;
 XX antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
 XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 XX cholesterol ester storage; systemic lupus erythematosus; infection;
 XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 XX bone damage; cartilage damage; antineoplastic disease; coagulation;
 XX thrombosis; contraceptive.

OS Homo sapiens.

PN W0200056473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US008621.

PR 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.

XX Shinketsu RA, Leach M;

XX WPI, 2000-602362/57.

DR N-PSDB; AAC75216.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.

PS Claim 11; Page 1266; 5507pp; English.
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397.

CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytoskeletal; hepatotropic; vulnary;
 CC antiproliferative; antiparkinsonian; neurotrophic; neuroprotective; osteopathic;
 CC anticonvulsant; antidiabetic; immunosuppressant; immunostimulant;
 CC cardiatic; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antihemetic; antihypertensive; antidiabetic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive

SO Sequence 57 AA:

Query Match 52.4%; Score 323; DB 3; Length 57;
 Best Local Similarity 100.0%; Pred. No. 3.4e-30;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

54 IECQANQASATSECTVAMGVCNHAFFHCISRWLKTQVCPDLNREWEFOKXGH 108
 Db 3 IECQANQASATSECTVAMGVCNHAFFHCISRWLKTQVCPDLNREWEFOKXGH 57

RESULT 13
 AAY06492
 ID AAY06492 standard; protein: 113 AA.
 XX
 AC AAY06492;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE Human sensitive to apoptosis (SAG) protein.
 XX
 KM SAG protein; sensitive to apoptosis; human; cancer; tumour;
 KM neurodegenerative disease; muscular dystrophy; wound healing; vulnary;
 KM therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 16..27
 FT Binding-site /note="prokaryotic membrane lipoprotein lipid attachment
 FT site"
 FT 47..51
 FT Binding-site /note="haem binding site"
 FT 49..66
 FT Region /note="somatotropin, prolactin and related hormone
 FT motif"
 FT 50..54
 FT Binding-site /note="haem binding protein"
 FT 54..63
 FT Region /note="aminoacyl-tRNA class II motif"
 FT 65..107
 FT Domain /note="Ly-6/U-par domain"
 FT 85..107
 FT Region /note="Kazal serine protease inhibitor motif"
 XX
 PN WO9932514-A2.
 XX
 XX 01-JUL-1999.
 PD
 XX 15-DEC-1998; 98MO-US026705.
 XX
 PF 19-DEC-1997; 97US-0068179P.
 XX
 PR 11-SEP-1998; 98US-0099840P.
 PD

XX (WARN) WARNER LAMBERT CO.
 PA
 XX
 XX Sun Y;
 PI
 XX
 XX WPI; 1999-430152/56.
 DR N-PSDB; AAX87314.
 DR
 XX
 PT SAG: Sensitive to Apoptosis Gene and related proteins, useful for
 PT promoting cell growth and protecting cells against apoptosis.
 XX
 XX Claim 20; Page 51-52; 84pp; English.
 PS
 XX
 XX This sequence represents a novel human redox-sensitive, haem-binding
 CC protein with a zinc RING finger domain that is encoded by the SAG gene
 CC (see AAX87314). SAG promotes cell growth, protects cells from apoptosis,
 CC scavenges oxygen radicals and can be used for the reversion of a tumour
 CC phenotype. SAG is highly conserved among species. Disruption in Yeast was
 CC shown to be lethal. SAG deletion mutants (see AAX87315-16) have been
 CC identified in human cancer lines, suggesting a role in carcinogenesis.
 CC SAG genes, and mutant SAG genes, can be used to protect cells from
 CC apoptosis induced by redox reagents. Antisense SAG genes can be used to
 CC inhibit the growth of tumour cells. The SAG genes can also be used for
 CC the recombinant production of the SAG proteins. The SAG proteins can be
 CC used to scavenge oxygen radicals in organisms and to promote wound
 CC healing. They are also ideal molecular targets in the development of
 CC drugs against neurodegenerative disorders, cancers and muscle dystrophy

SO Sequence 113 AA:

Query Match 47.4%; Score 292; DB 2; Length 113;
 Best Local Similarity 50.5%; Pred. No. 3.3e-26;
 Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;

11 SGTNSGAKGRFEYKKNVAVLWMDIYVDMCAICGNHIMDLIECQANQASATSECTV 70
 Db 20 SGRKSG-GDKVFSIKKNVAVLWMDIYVDMCAICGNHIMDLIECQANQASATSECTV 75
 QY 71 AMGVCHNAFFHCISRWLKTQVCPDLNREWEFOKXGH 107
 Db 76 VMGECNHSFFHCISRWLKTQVCPDLNREWEFOKXGH 112

RESULT 14
 AAB43295
 ID AAB43295 standard; protein: 113 AA.
 XX
 AC AAB43295;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF3059 polypeptide sequence SEQ ID NO:6118.
 XX
 XX Human; open reading frame; ORFX; detection; cytoskeletal; hepatotropic;
 KM vulnary; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
 KM anticonvulsant; osteopathic; antidiabetic; immunosuppressant; cardiatic;
 KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KM antiviral; antibacterial; antihemetic; antihypertensive; antidiabetic.
 KM antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KM cholesterol ester storage; systemic lupus erythematosus; infection;
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KM thrombosis; contraceptive.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200058473-A2.
 PN
 XX
 PD 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008621.
 XX 31-MAR-1999; 99US-0127607P.
 PR 02-APR-1999; 99US-0127636P.
 PR 05-APR-1999; 99US-0127728P.
 PR 30-MAR-2000; 2000US-00540763.
 XX (CURA-) CURAGEN CORP.
 XX Shimkets RA, Leach M;
 DR WPI, 2000-602362/57.
 DR N-PSDB; AAC77504.
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.
 PS Claim 11; Page 5300-5301; 5507pp; English.
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORF open reading frames 1 to 3161. The ORF
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerrary;
 CC antiproliferative; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antihypertensive; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatologic; immunosuppressive; antinflammatory; antibacterial;
 CC antiviral; antifungal; antihelmatic; antihydrolytic; and antianemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORF-associated disorder. The nucleic acids can be used to express ORF
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX Sequence 113 AA;
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 Query Match 47.4%; Score 292; DB 3; Length 113;
 Best Local Similarity 50.5%; Pred. No. 3.3e-26;
 Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;
 QY 11 SGTNSGAKRKFVKKNNALVLMMDIVDNCACRHHIMDLTECCONQASATSECTV 70
 DB 20 SSSKSG-GDKMPSLKKNNAVMAWMSWDVCDTCALCRVWDACLRQEN---KQEDCV 75
 QY 71 AMGVCHAHFHFCISRLKTRQVCPIDNREWEFOYCYG 107
 DB 76 VMGECHSHFHCNCSLWVKNNRCPLCQDDWVVGIG 112
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 AAU15873
 ID AAU15873 standard; protein; 118 AA.
 AC AAU15873;
 XX 07-NOV-2001 (first entry)
 XX Human novel secreted protein, Seq ID 826.
 DB Human; immunosuppressive; antihypertensive; antirheumatic; cytostatic;
 KW Human; immunosuppressive; antihypertensive; antirheumatic; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; vitucide; fungicide; ophthalmological; vulnerrary;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angiogenesis; nervous system disorder;

KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;
 KW preservative; antiproliferative.
 OS Homo sapiens.
 PN MO200155322-A2.
 XX 02-AUG-2001.
 XX 17-JAN-2001; 2001WO-US001341.
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
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 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
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 PR 28-JUN-2000; 2000US-0214886P.
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 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
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 PR 14-AUG-2000; 2000US-0225269P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
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PR 02-OCT-2000; 2000US-0237037P.
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PR 08-NOV-2000; 2000US-0246527P.
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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251866P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251899P.
PR 08-DEC-2000; 2000US-0251990P.

PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM,
XX
XX WPI, 2001-488783/53.
DR N-PSDB; AAS25860.
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 11, SEQ ID NO 826; 980pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC allelating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamin,
CC minerals, cofactors and other nutritional components. The present
CC sequence represents a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed

Query Match 47.4%; Score 292; DB 4; Length 118;
Best Local Similarity 50.5%; Pred. No. 3.5e-26;
Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;
QY 11 SGTNSGAGKKRFEVKKWNAVALMADIVDNCALICNHIIMDICTEQANQASATSECTV 70
Db 25 SGRKSG-GDKMPSLKKKNNAVAMWSVDECTCAICRVQWMDLRCQARN--KQBDVV 80
QY 71 AMGVCHAFHFHICISRLKTRQVCPLDNREWERQKYG 107
Db 81 VMGCHNSFHNCCMSLWKNRCPLOCDDWVQRIIG 117

Search completed: March 25, 2004, 09:34:45
Job time : 55 secs

Thu Mar 25 10:42:32 2004

us-09-914-324a-1.rat

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:33:42 : Search time 22 Seconds
(without alignments)
25.437 Million cell updates/sec

Title: US-09-914-324a-1

Perfect score: 616

Sequence: 1 MAAMADVDPSTGNSAGKK.....KTRQVCPIDNREWEFOYVGH 108

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	208	33.8	84	US-09-599-360B-77	Sequence 77, App1
2	185	30.0	112	US-09-621-976-5677	Sequence 5677, Ap
3	185	30.0	112	US-09-621-976-5805	Sequence 5805, Ap
4	105.5	17.1	94	US-09-621-976-5714	Sequence 5714, Ap
5	85	13.8	664	US-09-268-140-2	Sequence 2, App1
6	83	13.5	104	US-09-325-932A-49	Sequence 49, App1
7	83	13.5	337	US-09-828-303-18	Sequence 18, App1
8	80	13.0	180	US-08-786-606-3	Sequence 3, App1
9	80	13.0	180	US-08-933-750C-48	Sequence 48, App1
10	80	13.0	180	US-09-234-613-48	Sequence 48, App1
11	80	13.0	284	US-08-786-606-9	Sequence 9, App1
12	79	12.8	50	US-09-053-089A-15	Sequence 15, App1
13	79	12.8	359	US-09-663-600A-106	Sequence 106, App
14	79	12.8	381	US-08-867-057-1	Sequence 1, App1
15	79	12.8	381	US-08-867-057-3	Sequence 3, App1
16	79	12.8	381	US-09-128-369-1	Sequence 1, App1
17	79	12.8	381	US-09-128-369-3	Sequence 3, App1
18	79	12.8	381	US-09-663-600A-700	Sequence 200, App
19	79	12.8	410	US-07-945-283-4	Sequence 4, App1
20	76.5	12.4	317	US-09-921-099A-8	Sequence 8, App1
21	76	12.3	1302	US-09-423-890-2	Sequence 2, App1
22	76	12.3	1493	US-09-423-890-8	Sequence 8, App1
23	76	12.3	1593	US-08-628-828-4	Sequence 4, App1
24	75.5	12.3	305	US-08-628-828-8	Sequence 114, App
25	74.5	12.1	67	US-07-945-283-5	Sequence 5, App1
26	74.5	12.1	149	US-09-690-454-205	Sequence 205, App
27	74.5	12.1	166	US-09-690-454-204	Sequence 204, App

28	74.5	12.1	826	US-09-894-998A-47	Sequence 47, App1
29	73	11.9	551	US-08-699-103B-25	Sequence 25, App1
30	73	11.9	551	US-09-229-059-25	Sequence 25, App1
31	73	11.9	551	US-09-628-133-25	Sequence 25, App1
32	72.5	11.8	66	US-09-205-258-1030	Sequence 1030, App
33	72.5	11.8	69	US-07-945-283-6	Sequence 6, App1
34	72.5	11.8	84	US-09-205-258-1032	Sequence 1032, App
35	72.5	11.8	167	US-09-205-258-1026	Sequence 1026, App
36	72.5	11.8	276	US-08-786-606-5	Sequence 5, App1
37	72.5	11.8	276	US-09-205-258-1027	Sequence 1027, App
38	72.5	11.8	341	US-09-205-258-1034	Sequence 1034, App
39	71	11.5	40	US-09-046-894-44	Sequence 44, App1
40	71	11.5	199	US-09-325-932A-46	Sequence 46, App1
41	70.5	11.4	46	US-08-691-814B-17	Sequence 17, App1
42	67.5	11.0	49	US-09-230-637-60	Sequence 60, App1
43	67	10.9	395	US-08-841-349-9	Sequence 9, App1
44	67	10.9	395	US-09-431-184A-9	Sequence 9, App1
45	66	10.7	67	US-07-945-283-7	Sequence 7, App1

ALIGNMENTS

RESULT 1
US-09-599-360B-77
Sequence 77, Application US/09599360B
Patent No. 654833
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bouquelieret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET.060C93
CURRENT APPLICATION NUMBER: US/09/599,360B
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113, 666
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141, 032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469, 099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 77
LENGTH: 84
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-599-360B-77

Query Match 33.8%, Score 208; DB 4; Length 84;
Best Local Similarity 37.5%; Pred. No. 1, 1e-15;
Matches 33; Conservative 17; Mismatches 30; Indels 8; Gaps 2;

QY 21 RFEVKMNAVALMADIVDNCALCRNIMDLCTECQANQASTSECTVAMGVCHNATH 80
DB 2 KYKIKCMNGVATWLMVANDRCGICRMAFNGCCPDCR---VPGDDCPILWQCSCHPH 56
QY 81 FHCISRWLKTQV---CPIDNREWEFOK 105
DB 57 MHCITKMLAQVQCHRCMCRGWEKFE 84

RESULT 2
US-09-621-976-5677
Sequence 5677, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Gobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976

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;; CURRENT FILING DATE: 2000-07-21
;; NUMBER OF SEQ ID NOS: 19335
;; SOFTWARE: Patent.pm
;; SEQ ID NO 5677
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -106...-1
US-09-621-976-5677

Query Match
Best Local Similarity 30.0%; Score 185; DB 4; Length 112;
Best Local Similarity 38.0%; Pred. No. 5.1e-13;
Matches 30; Conservative 13; Mismatches 28; Indels 8; Gaps 2;

QY 21 REEVKKNVAVLAWMDIVVNCALICRNHIMDLCECOANQASATSECTVAMGVCHAFH 80
DB 2 KYKIKCMGVATWLVWANDENCGICRMAFNGCCPDCK-----VGDGDCPLVWGQCSCHF 56
QY 81 FHCISRMLKTRGV---CPL 96
DB 57 MHCILKMLHAQVQCHCPM 75

RESULT 3
US-09-621-976-5805
;; Sequence 5805, Application US/09621976
;; Patent No. 6639063
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, J.B.
;; APPLICANT: Jobert, S.
;; APPLICANT: Giordano, J.Y.
;; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;; FILE REFERENCE: GENSET.054PR2
;; CURRENT APPLICATION NUMBER: US/09/621,976
;; CURRENT FILING DATE: 2000-07-21
;; NUMBER OF SEQ ID NOS: 19335
;; SOFTWARE: Patent.pm
;; SEQ ID NO 5805
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -109...-1
US-09-621-976-5805

Query Match
Best Local Similarity 30.0%; Score 185; DB 4; Length 112;
Best Local Similarity 38.0%; Pred. No. 5.1e-13;
Matches 30; Conservative 13; Mismatches 28; Indels 8; Gaps 2;

QY 21 REEVKKNVAVLAWMDIVVNCALICRNHIMDLCECOANQASATSECTVAMGVCHAFH 80
DB 2 KYKIKCMGVATWLVWANDENCGICRMAFNGCCPDCK-----VGDGDCPLVWGQCSCHF 56
QY 81 FHCISRMLKTRGV---CPL 96
DB 57 MHCILKMLHAQVQCHCPM 75

RESULT 4
US-09-621-976-5714
;; Sequence 5714, Application US/09621976
;; Patent No. 6639063
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, J.B.
;; APPLICANT: Jobert, S.
;; APPLICANT: Giordano, J.Y.
;; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;; FILE REFERENCE: GENSET.054PR2
;; CURRENT APPLICATION NUMBER: US/09/621,976
;; CURRENT FILING DATE: 2000-07-21

;; NUMBER OF SEQ ID NOS: 19335
;; SOFTWARE: Patent.pm
;; SEQ ID NO 5714
;; LENGTH: 94
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -53...-1
;; NAME/KEY: UNSURE
;; LOCATION: 14
;; OTHER INFORMATION: Xaa = Glu, Gln
US-09-621-976-5714

Query Match
Best Local Similarity 17.1%; Score 105.5; DB 4; Length 94;
Best Local Similarity 36.6%; Pred. No. 0.00022;
Matches 15; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

QY 48 HIMDLCECOANQASATSECTVAMGVCHAFHFCISRML 88
DB 10 HLTDAAPDCK-----VGDGDCPLVWGQCSCHFIMHILKWL 45

RESULT 5
US-09-268-140-2
;; Sequence 2, Application US/09268140
;; Patent No. 6268176
;; GENERAL INFORMATION:
;; APPLICANT: Gemmill, Robert M.
;; APPLICANT: Dyabkin, Harry A.
;; TITLE OF INVENTION: TRCS, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
;; FILE REFERENCE: 93445-00004
;; CURRENT APPLICATION NUMBER: US/09/268,140
;; CURRENT FILING DATE: 2000-03-12
;; PRIOR APPLICATION NUMBER: US 60/077,723
;; PRIOR FILING DATE: 1998-03-12
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 664
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-268-140-2

Query Match
Best Local Similarity 13.8%; Score 85; DB 3; Length 664;
Best Local Similarity 28.6%; Pred. No. 0.34; 22; Indels 28; Gaps 4;
Matches 24; Conservative 10; Mismatches 13

QY 20 REEVKKNVAVLAWMDI-----VVDNCAICRNHIMDLCECOANQASATSECTVAM 72
DB 522 RRTAVKINSIP---EIKSRLQEIINDVCAICYHF-----TTSARIT--- 561
QY 73 GVCNHAFFHICISRMLKTRGVCP 96
DB 562 PCNHYFHALCIRKMLYIQDTCM 584

RESULT 6
US-09-325-932A-49
;; Sequence 49, Application US/09325932A
;; Patent No. 6451604
;; GENERAL INFORMATION:
;; APPLICANT: Flinn, Barry
;; APPLICANT: Lasham, Annette
;; TITLE OF INVENTION: Compositions affecting programmed cell
;; FILE REFERENCE: 1022
;; CURRENT APPLICATION NUMBER: US/09/325,932A
;; CURRENT FILING DATE: 1999-06-04
;; NUMBER OF SEQ ID NOS: 206
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 49
;; LENGTH: 104

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us-09-914-324a-1.ra1

Page 3

TYPE: PRT
ORGANISM: Pinus radiata
US-09-325-932A-49

Query Match 13.5%; Score 83; DB 4; Length 104;
Best Local Similarity 30.9%; Pred. No. 0.071;
Matches 17; Conservative 4; Mismatches 20; Indels 14; Gaps 1;

QY 42 CAICRNHMDICIEQANQASATSECTVANGVCNHAFFHCISRMLKTRQVCP 96
DB 25 CAVCLSKFEDI-----EILRLPKCRHAFHIDCIDVWLEKHSKCP 65

RESULT 7
US-09-828-303-18
Sequence 18, Application US/09828303
Patent No. 6677504
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNER, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: TRANSCRIPTION FACTOR STRESS-RELATED PROTEINS AND
METHODS OF USE IN PLANTS
FILE REFERENCE: 16313-0030
CURRENT APPLICATION NUMBER: US/09/828,303
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 18
LENGTH: 337
TYPE: PRT
ORGANISM: Physcomitrella patens
US-09-828-303-18

Query Match 13.5%; Score 83; DB 4; Length 337;
Best Local Similarity 29.3%; Pred. No. 0.27;
Matches 17; Conservative 7; Mismatches 20; Indels 14; Gaps 2;

QY 39 VDNCAICRNHMDICIEQANQASATSECTVANGVCNHAFFHCISRMLKTRQVCP 96
DB 85 VEFCAVCL-----EFLGKGRKTLRK-----CHSHFLDCIDVWLEKHSKCP 128

RESULT 8
US-08-786-606-3
Sequence 3, Application US/08786606
Patent No. 5861495
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Coleman, Roger
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,606
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy R
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0173 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-786-606-3

Query Match 13.0%; Score 60; DB 2; Length 180;
Best Local Similarity 28.2%; Pred. No. 0.28;
Matches 29; Conservative 12; Mismatches 18; Indels 44; Gaps 7;

QY 1 MAANDVD-TPSGTN--SGAGKRFVKKNAVALAMWDIVDNCAICRNHMDICIEC 56
DB 1 MAAREEDGCEGPRERGGAG-ATFE-----CNICILE-32

QY 57 QANQASATSECTVANGVCNHAFFHCISRMLKT---ROYCP 96
DB 33 -----TAREAVYS--VGHLYCWPCLHQLWLETRPSRQCPV 66

RESULT 9
US-08-933-750C-48
Sequence 48, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTNOT07
CLONE: 3217567
US-08-933-750C-48

Query Match 13.0%; Score 80; DB 2; Length 180;
Best Local Similarity 28.2%; Pred. No. 0.28; Indels 44; Gaps 7;
Matches 29; Conservative 12; Mismatches 18; Indels 44; Gaps 7;

QY 1 MAAAMDVD-TPSGTN---SGAGKREPEVKMNAVALMAMDIVDNCALCRNHIMDLICRC 56
DB 1 MAAAEEDGGPEGPNNRERGAG-ATPE-----CNICLE- 32
QY 57 QANQASATSECTVANGVCNHAFFHCISRMLKT---RQVCPL 96
DB 33 -----TAREAVVS--VCGHLYCWPCLHQLWLETREROCEPV 66

RESULT 10
US-09-234-613-48
Sequence 48, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTNOT07
CLONE: 3217567
US-09-234-613-48

Query Match 13.0%; Score 80; DB 3; Length 180;
Best Local Similarity 28.2%; Pred. No. 0.28; Indels 44; Gaps 7;
Matches 29; Conservative 12; Mismatches 18; Indels 44; Gaps 7;

QY 1 MAAAMDVD-TPSGTN---SGAGKREPEVKMNAVALMAMDIVDNCALCRNHIMDLICRC 56
DB 1 MAAAEEDGGPEGPNNRERGAG-ATPE-----CNICLE- 32
QY 57 QANQASATSECTVANGVCNHAFFHCISRMLKT---RQVCPL 96
DB 33 -----TAREAVVS--VCGHLYCWPCLHQLWLETREROCEPV 66

RESULT 11
US-08-786-606-9
Sequence 9, Application US/08786606
Patent No. 5861495
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Coleman, Roger
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,606
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0173 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 157535
US-08-786-606-9
Query Match 13.0%; Score 80; DB 2; Length 284;
Best Local Similarity 25.5%; Pred. No. 0.47; Indels 32; Gaps 3;
Matches 24; Conservative 9; Mismatches 29; Indels 32; Gaps 3;

Thu Mar 25 10:42:32 2004

us-09-914-324a-1.ra1

Page 5

QY 3 AANDVTPSGTSGAGKKEFEVKKNAVALMAMDIYVNCALCRHIMDLCEQANQAS 62
Db 104 AAKMIPKTKG-----KPSDEK-----DLSDCCALC-----1E 131
QY 63 ATSECTVAMGVCMNAFHFCISRWLKTROVCP 96
Db 132 AKKPTIRILPCGHEPHKNCIDPWLJHRTCM 165

RESULT 12

US-09-052-089A-15
Sequence 15, Application US/09052089A
Patent No. 6346605
GENERAL INFORMATION:
APPLICANT: Lee, Soo Y.
Choi, Yongwon
TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE TGF RECEPTOR SUPER
FAMILY, AND USES THEREOF
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Application Number: US/09/052,089A
FILING DATE: 31-Mar-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-052-089A-15
Query Match 12.8%; Score 79; DB 4; Length 50;
Best Local Similarity 29.3%; Pred. No. 0.085; 15; Indels 16; Gaps 3;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;
QY 40 DNCAICRNHIMDLCEQANQASATSECTVAMGVCMNAFHFCISRWL-KTROVCP 96
Db 2 DVCAICLDEYED-----GDKRLRL-PCSHAYHCKVDPWLTKTKTCV 44

RESULT 13

US-09-663-600A-106
Sequence 106, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bouguetier, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A

CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 106
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -34...-1
NAME/KEY: UNSURE
LOCATION: 20,64,65,130,156,282,288,289,294,296,300,302,310
OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-09-663-600A-106

Query Match 12.8%; Score 79; DB 4; Length 359;
Best Local Similarity 29.3%; Pred. No. 0.78; 15; Indels 16; Gaps 3;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;
QY 40 DNCAICRNHIMDLCEQANQASATSECTVAMGVCMNAFHFCISRWL-KTROVCP 96
Db 238 DVCAICLDEYED-----GDKRLRL-PCSHAYHCKVDPWLTKTKTCV 280

RESULT 14

US-08-867-057-1
Sequence 1, Application US/08867057
Patent No. 5840535
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lai, Preeti
APPLICANT: Shah, Puryi
TITLE OF INVENTION: NEW ZINC RING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
Application Number: US/08/867,057
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0311 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: EMBL02
CLONE: 104119
US-08-867-057-1

Query Match 12.8%; Score 79; DB 2; Length 381;
Best Local Similarity 29.3%; Pred. No. 0.84;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;

QY 40 DNCAICGNHIMDLCEQANQASATSECTVAMGVCNHAFFHCISRWL-KTROVCP 96
DB 238 DVCAICIDEYED-----GDKLRIL--PCHAHCKCVDPMILTKTKTCPPV 280

RESULT 15

US-08-867-057-3
Sequence 3, Application US/08867057
Patent No. 5840535
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Parvi
TITLE OF INVENTION: NEW ZINC RING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,057
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0311 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1321818
US-08-867-057-3

Query Match 12.8%; Score 79; DB 2; Length 381;
Best Local Similarity 29.3%; Pred. No. 0.84;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;

QY 40 DNCAICGNHIMDLCEQANQASATSECTVAMGVCNHAFFHCISRWL-KTROVCP 96

DB 238 DVCAICIDEYED-----GDKLRIL--PCHAHCKCVDPMILTKTKTCPPV 280

Search completed: March 25, 2004, 09:37:17
Job time : 23 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: March 25, 2004, 09:31:32 ; Search time 39 Seconds
(without alignments)
873.743 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMADYDTSGTSGNAGAKK.....KTRQVCPDNRWEPQKRGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP viirus: *
16: SP bacteriap: *
17: SP archaep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523.5	85.0	114	10	Q863S0
2	523	84.9	110	10	Q7Y042
3	378	61.4	107	5	Q77367
4	314.5	51.1	97	10	Q9FTN1
5	308	50.0	92	5	Q8SW76
6	284.5	46.2	113	5	Q9V607
7	266	43.2	112	5	P91404
8	210	34.1	84	10	Q940X6
9	198	32.0	85	5	Q9VLU5
10	197	32.1	85	5	Q8IC8
11	151	24.5	135	5	Q20052
12	146.5	23.8	57	10	Q9W9L0
13	141	22.9	165	3	Q12157
14	136	22.1	99	10	Q9AVZ5
15	132.5	21.5	94	3	Q86ZL9
16	129.5	21.0	94	3	Q86ZL9

17	116.5	18.9	2160	5	Q17709	Q17709 caenorhabdi
18	112.5	18.3	911	3	Q66TDS	Q66TDS neurospora
19	106.5	17.3	189	10	Q84U02	Q84U02 cryza sativ
20	106	17.2	445	12	Q8QK70	Q8QK70 ectocarpus
21	104	16.9	349	10	Q8U066	Q8U066 arabidopsis
22	104	16.9	693	5	Q8U17	Q8U17 clona intes
23	102.5	16.6	249	10	Q9CASS	Q9CASS arabidopsis
24	102	16.6	151	10	Q9F195	Q9F195 arabidopsis
25	102	16.6	210	10	Q9SD55	Q9SD55 arabidopsis
26	100	16.2	147	10	Q9LTV5	Q9LTV5 arabidopsis
27	100	16.2	650	10	Q84W43	Q84W43 arabidopsis
28	100	16.2	676	10	Q9M152	Q9M152 arabidopsis
29	99.5	16.2	207	5	Q7Y15	Q7Y15 cryptospori
30	98	15.9	147	10	Q84W41	Q84W41 cryza sativ
31	98	15.8	158	10	Q9SRM0	Q9SRM0 arabidopsis
32	97.5	15.8	272	10	Q9FHA1	Q9FHA1 arabidopsis
33	97	15.7	159	10	Q8LZV8	Q8LZV8 arabidopsis
34	97	15.7	295	10	Q8H740	Q8H740 medicago sa
35	97	15.7	327	10	Q9C711	Q9C711 arabidopsis
36	96	15.6	332	10	Q9LQW2	Q9LQW2 arabidopsis
37	95.5	15.5	233	10	Q9FSZ7	Q9FSZ7 cicier arlet
38	95.5	15.5	291	10	Q9SR08	Q9SR08 arabidopsis
39	95.5	15.5	356	10	Q9SS58	Q9SS58 arabidopsis
40	95.5	15.5	383	10	Q7XLY9	Q7XLY9 cryza sativ
41	95.5	15.5	441	10	Q3J446	Q3J446 arabidopsis
42	95	15.4	227	10	Q8LJB8	Q8LJB8 cryza sativ
43	95	15.4	322	10	Q9SMQ0	Q9SMQ0 arabidopsis
44	95	15.4	336	12	Q9VVP5	Q9VVP5 melampoplus
45	95	15.4	362	10	Q9LF64	Q9LF64 arabidopsis

ALIGNMENTS

RESULT 1

Q863S0 PRELIMINARY; PRT; 114 AA.

AC Q863S0; 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative ring box-1 protein.
GN 49P11.12.
OS Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae;
OC Ethnarcoidae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare; Ramakrishna W., Sam Miguel P., Shiloff B.,
RA Park Y.-U., Koshino N., Ma J., Jiang Z., Kleinholz A., Bennettzen J.,
RT "Sequence characterization of orthologous regions in the barley and
RT rice genomes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480496; ALB67158.1; -
DR Gramene; Q863S0; -
DR InterPro; IPR001841; Znf_ring.
DR SMART; PF00097; zf-GHCA; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PSS0089; ZF_RING_2; 1.
SQ SEQUENCE 114 AA; 12754 MW; 568C63E0D733D5C CRC64;

Query Match

Best Local Similarity 84.4% ; Score 523.5; DB 10; Length 114;
Matches 92; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAAMADYDTSGTSGNAGAKK-KREFVKKMAVALAMADIVDNCALCNHIMDLCTICEOAN 59
DB 6 VAVAVPSSINAGASSGAKKGRFEIKKNVSLWAMDIVDNCALCNHIMDLCTICEOAN 65
QY 60 QASATSECTVAMGVCHAFHFHCISRWLKTROVCPDNRWEPQKRGH 108

Db 66 QASATSECTVAMGVCNHAHFHFCISRMLKTRQVCPDLNDEWEFQYXGH 114

RESULT 2

Q7Y042 PRELIMINARY; PRT; 110 AA.
 AC Q7Y042;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Ring box protein.
 OS Populus tomentosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 CX NCBI_TaxID=118781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fan J.H.;
 RT "Ring-box protein (PUBX1) of Populus tomentosa."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY02066; AAP57304.1; -
 SQ SEQUENCE 110 AA; 12591 MW; 0172C6CAE3FA2772 CRC64;

Query Match 84.9%; Score 523; DB 10; Length 110;
 Best Local Similarity 84.5%; Pred. No. 3.3e-55;
 Matches 93; Conservative 4; Mismatches 7; Indels 6; Gaps 2;

QY 5 MDVYD--TTPSG--TNSGAKKPEFEVKKNVAVALMWDIVDNCALCRNHIMDLCECOA 58
 Db 1 MDIVTMVPAAGEASSSSSRKPKREIKKNVAVALMWDIVDNCALCRNHIMDLCECOA 60

QY 59 NQASATSECTVAMGVCNHAHFHFCISRMLKTRQVCPDLNDEWEFQYXGH 108
 Db 61 NQASATSECTVAMGVCNHAHFHFCISRMLKTRQVCPDLNDEWEFQYXGH 110

RESULT 3

Q77367 PRELIMINARY; PRT; 107 AA.

AC Q77367;
 DT 01-NOV-1998 (TREMBlrel. 09, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Putative ring finger protein.

GN MAJ3P6.28. falciparum (isolate 3D7).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 CX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 11
 RC STRAIN=3D7;
 RC MEDLINE=99376085; PubMed=1048855;

RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
 RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
 RA Gentles S., Gilliam R., Hamlin N., Harris D., Holtroyd S., Hornsby T.,
 RA Horrocks P., Jagsal K., Jagsal B., Kyes S., McLean U., Moulé S.,
 RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
 RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
 RA Whitehead S., Woodward J.R., Newbold C., Barrall B.G.;
 RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
 falciparum.";
 RL Nature 400:532-538 (1999).
 DR EMBL: Z98551; CAB1123.3; -
 DR PIR: T18513; T18513.
 DR InterPro: IPR01841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4_1.
 DR SMART: SM00184; RING_1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 107 AA; 12419 MW; C563432A60F20262 CRC64;

Query Match 61.4%; Score 378; DB 5; Length 107;

Best Local Similarity 69.6%; Pred. No. 9.3e-38;
 Matches 64; Conservative 5; Mismatches 15; Indels 8; Gaps 1;

QY 22 FEVKKNVAVALMWDIVDNCALCRNHIMDLCECOA-----NQASATSECTVAMG 73

Db 13 FKHKMSAVAMSWDIDVNDNCALCRNHIMDLCECAKTTDHNKDKIKDKGCTVAMG 72

QY 74 VCNHAFHFCISRMLKTRQVCPDLNDEWEFQYXGH 105

Db 73 VCNHAFHFCISRMLKTRQVCPDLNDEWEFQYXGH 104

RESULT 4

Q9FTN1 PRELIMINARY; PRT; 97 AA.

AC Q9FTN1;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE P005A05.18 protein (P0482C06.1 protein).
 GN Oryza sativa (Rice).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.

CX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsunoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P005A05.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

QY 12
 RC STRAIN=CV. Nipponbare;
 RC Sasaki T., Matsunoto T., Yamamoto K.;
 RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0482C06.";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP002863; BAB16914.1; -
 DR EMBL: AP002845; BAB78605.1; -
 DR Gramene: Q9FTN1; -
 SQ SEQUENCE 97 AA; 10329 MW; F6DD1CE7BEDBA579 CRC64;

Query Match 51.1%; Score 314.5; DB 10; Length 97;
 Best Local Similarity 69.4%; Pred. No. 3.8e-30;
 Matches 59; Conservative 5; Mismatches 4; Indels 17; Gaps 2;

QY 6 DVDTP-----SGTNSGAG-----KKFEVKKNVAVALMWDIVDNCALCRNH 48
 Db 4 DINAPPPAPAPAGAGGSSSAAGSSSRKPKREIKKNVAVALMWDIVDNCALCRNH 63

QY 49 IMDLCIECOANQASATSECTVAMG 73
 Db 64 IMDLCIECOANQASATSECTVAMG 88

QY 49 IMDLCIECOANQASATSECTVAMG 73
 Db 64 IMDLCIECOANQASATSECTVAMG 88

RESULT 5

Q8SWU6 PRELIMINARY; PRT; 92 AA.

AC Q8SWU6;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein ECU01_1095.
 GN ECU01_1095.
 OS Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.

OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
 CX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.

Query Match 61.4%; Score 378; DB 5; Length 107;

RA Genoscope;
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RC SEQUENCE FROM N.A.
 RP STRAIN=GB-M1;
 RX MEDLINE=21576510; PubMed=11719806;
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Premsier G., Barde V., Peyretallade E., Broctier P., Winkler P.,
 RA Delac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vavres C.F.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT "Encephalitozoon cuniculi";
 RT Nature 414:450-453(2001).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AJ391737; CDD24981.1; -;
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; Zf-CHC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KM Hypochemical protein; Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 92 AA; 10807 MW; 2B04FBEAF093084 CRC64;

Query Match 50.0%; Score 308; DB 5; Length 92;
 Best Local Similarity 56.5%; Pred. No. 2,2e-29;
 Matches 48; Conservative 16; Mismatches 19; Indels 2; Gaps 1;

QY 19 KKRFEVKNNVAVALMWDIVDNCALCRHINDLCIECOANQASATSECTVANGVCNHA 78
 Db 4 KEIKLKKNMVALMELDKMKIERCALCRHINDTCVECG--NGMTNGSCKSNQVCNHA 61
 QY 79 FFEHCISRMKTRQVCPDLDNREMEF 103
 Db 62 FHTHCITRMLSKNVCPDLDTKKVVY 86

RESULT 6
 QY607 PRELIMINARY; PRT; 113 AA.
 AC QY607;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE CG8998 protein (R81847p).
 OS CG8998.
 GN Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballou R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkov D., Borchan M.R., Bouck J., Brokstein P., Broctier P.,
 RA Burris J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos M., Delcher A., Deng Z., Meyers A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.B., Downes K., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RP Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Barzon J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Fafian D.,
 RA Ferrleria S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibsgen C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Patel J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Procinik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman D., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mangall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A.
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RN SEQUENCE FROM N.A.
 RP Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkeley;
 RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Fafian D., Frise E.,
 RA George R., Gonzalez M., Guarini H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF003825; AA558633.2; -;
 DR EMBL; AY13544; AA29549.1; -;
 DR Flybase; FBgn003641; CG8998.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; Zf-CHC4; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 113 AA; 13101 MW; 41F16639A2EC1252 CRC64;

Query Match 46.2%; Score 284.5; DB 5; Length 113;

Matches 30; Conservative 20; Mismatches 29; Indels 8; Gaps 2;

QY 21 REEVKNNAAVLMADIVDNCATCRNIMDLCECCANQASATSECTVAMGVCHNAFFHC 80
 Db 2 KXKTLQMGVSWMNAODETGCIRMAFDGCCPCCK-----FEDDDCLPMGVCSCNAPFH 56
 QY 81 FHCISRWLKT---OVCPDNRNEMEQ 104
 Db 57 LHCLIKMWNVSOTSTPLCPCRCREMOFK 83

RESULT 10

QYVLJ5 PRELIMINARY; PRT; 85 AA.
 AC QYVLJ5; QYVLJ4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG18042 protein (putative Apc11 anaphase-promoting complex subunit).
 DE LMG OR CG18042.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter S.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abghyani A., An H.-Y., Andrews-Pfankuch C., Baldwin D.,
 RA Ballow R.M., Basu P.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu L.B., Davies P.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
 RA Fodor A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Golder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J., Q.A.,
 RA Williams S., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP Celnikier S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Bazzon J., An H., Baldwin D., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegam C., Jalali M., Kruse D., Li P., Matei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
 RA Paclob J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RT "Sequencing of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]
 RP SEQUENCE FROM N.A.
 RA Maier S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnikier S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnikier S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[5]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

[6]
 RP SEQUENCE FROM N.A.
 RA Taylor C.A., Shitras A.D.;
 RT "cell cycle arrest and apoptosis in lemming mutants of Drosophila melanogaster";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003621; AA052694.2;
 DR EMBL; AJ251510; CAB63945.1;
 DR Flybase; FB00029004; lmg.
 DR InterPro; IPR001841; znf_fing.
 DR PROSITE; PS50089; zfp_RING_2; 1.
 SQ SEQUENCE 85 AA; 9859 MW; 01EF449D32BEDBA2 CRC64;

Query Match 32.0%; Score 197; DB 5; Length 85;
 Best Local Similarity 37.3%; Pred. No. 5e-16;
 Matches 31; Conservative 13; Mismatches 31; Indels 8; Gaps 2;

QY 24 VKKNNAAVLMADIVDNCATCRNIMDLCECCANQASATSECTVAMGVCHNAFFHC 83
 Db 5 IKSWGVATWMIWINDENCGICRNSFSTCEPC-----ALPGDDCLPMGVCSCNAPFH 59
 QY 84 ISRWLKTROV---CPDNRNEMEQ 103
 Db 60 IVKMLNQLPLNKQCPMCRGQSWKF 82

RESULT 11

ID Q8IC8 PRELIMINARY; PRT; 89 AA.

AC Q8IC8;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DE Anaphase-promoting complex subunit, putative.

GN MAL6P1.184.
 OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=36329;

RN [1]
 RP SEQUENCE FROM N.A.
 RP Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
 RA Bettman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,

RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL844505; CAD50514.1; -;
DR InterPro: IPR001841; Znf_ring;
DR PROSITE: PSS0089; ZF_RING_2; 1;
SQ SEQUENCE 89 AA; 10211 MW; 1987493D9583BA23D CRC64;

Query Match 24.5%; Score 151; DB 5; Length 89;
Best Local Similarity 33.3%; Pred. No. 1.8e-10;
Matches 28; Conservative 16; Mismatches 32; Indels 8; Gaps 4;

QY 24 VKKNAVALMAW-DIVVDN-CALCRNHIMDLCTECQANQASATSECTVAMGVCHNAFHF 81
DB 6 VKRIHAAPRMKWTSTDSVCAICNSSELENTTTCM-----RPGNGCPPAFGKCHHFFL 60
QY 82 HCISRWLKTQGV-CPLDNRWEPQ 104
DB 61 HCMKMKIKONKLTCPCCRADWYE 84

RESULT 12
Q20052 PRELIMINARY; PRT; 135 AA.

ID Q20052
AC Q20052
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F35G12.9 protein.
GN F35G12.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6229;

RA [1]
RP SEQUENCE FROM N.A.
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=99069613; PubMed=9851916;

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018 (1998).
CC -1- SIMILARITY: CONTAINING 1 RING-TYPE ZINC FINGER.

DR EMBL: Z46242; CA86328.1; -;
DR PIR: T21802; T21802.CE00978.
DR WormPep: F35G12.9; CE00978.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SMO0184; RING; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
KW Metal-binding; zinc-finger.
SQ SEQUENCE 135 AA; 15512 MW; 1CC8B4AFLAB671E7 CRC64;

Query Match 23.8%; Score 146.5; DB 5; Length 135;
Best Local Similarity 33.3%; Pred. No. 1e-09;
Matches 28; Conservative 10; Mismatches 35; Indels 11; Gaps 3;

QY 24 VKKNAVALMAW-DIVVDN-CALCRNHIMDLCTECQANQASATSECTVAMGVCHNAFHF 82
DB 53 VKKLHVGEMKMLQGGEDTCGICMEFBSAC-----NMCKKFGDDCPVLGICRHAFFRH 107
QY 83 CISRWL-----KTRQVCPDNRW 101
DB 108 CIDKWIAPFTNPRAQCPDRCQDW 131

RESULT 13
Q9M9L0 PRELIMINARY; PRT; 57 AA.
AC Q9M9L0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F10A16.17 protein.
GN F10A16.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ev. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F10A16 genomic sequence."
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINING 1 RING-TYPE ZINC FINGER.
DR EMBL: AC012393; AAF26089.1; -;
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PR00097; zf-C3HC4; 1.
DR SMART: SMO0184; RING; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
KW Metal-binding; zinc; zinc-finger.
SQ SEQUENCE 57 AA; 6580 MW; 504C753B7B745C74 CRC64;

Query Match 22.9%; Score 141; DB 10; Length 57;
Best Local Similarity 41.1%; Pred. No. 1.8e-09;
Matches 23; Conservative 12; Mismatches 13; Indels 8; Gaps 3;

QY 53 CIECQANQASATSECTVAMGVCHNAFHFHCISRWL--KTRQV-CPLDNRWEPQ 105
DB 7 CPDCK-----LPGDCCPLIWGACNHAFFHLCLKWNVSQTSQAHCPGRREWQFKE 57

RESULT 14
Q12157 PRELIMINARY; PRT; 165 AA.

ID Q12157
AC Q12157;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chromosome IV reading frame ORF YDL008W.

GN APC11 OR D2800 OR YDL008W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

RA [1]
RP SEQUENCE FROM N.A.
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=99069613; PubMed=9851916;

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018 (1998).
CC -1- SIMILARITY: CONTAINING 1 RING-TYPE ZINC FINGER.

DR EMBL: Z74056; CA86328.1; -;
DR PIR: T21802; T21802.CE00978.
DR WormPep: F35G12.9; CE00978.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SMO0184; RING; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 165 AA; 18865 MW; 99F8B8C6B841934 CRC64;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 25, 2004, 09:25:22 ; Search time 17 seconds
(without alignments)
330.739 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMDVDPGSGTNSGAGK.....KTRQVCPUDNREMFQKXGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	108	1 RBX1_HUMAN	Q96268 homo sapien
2	614	98.1	108	1 RBX1_SALSA	Q89664 salmo salar
3	534	86.7	108	1 RBXA_DROME	Q94961 drosophila
4	514.5	83.5	118	1 RBXA_ARATH	Q940X7 arabidopsis
5	499	81.0	115	1 RBXB_ARATH	Q940B0 arabidopsis
6	493	80.0	110	1 RBX1_CAEL	Q23457 caenorhabdi
7	469	76.1	107	1 RBX1_MOUSE	Q13959 schizosacch
8	400.5	65.0	122	1 RBXB_DROME	Q940X0 drosophila
9	385	62.5	121	1 RBX1_YEAST	Q08273 saccharomyc
10	292	47.4	113	1 RBX2_HUMAN	Q940F6 homo sapien
11	290.5	47.2	113	1 RBX2_MOUSE	Q940F6 homo sapien
12	209	33.9	84	1 ANI1_MOUSE	Q940F6 homo sapien
13	208	33.8	84	1 ANI1_HUMAN	Q940F6 homo sapien
14	164.5	26.7	94	1 YTP3_SCHPO	Q940F6 homo sapien
15	91	14.8	148	1 RN24_HUMAN	Q940F6 homo sapien
16	90	14.6	600	1 RN12_MOUSE	Q940F6 homo sapien
17	88	14.3	161	1 YODD_CAEL	Q940F6 homo sapien
18	87	14.0	326	1 PEXA_HUMAN	Q940F6 homo sapien
19	86	14.0	326	1 PEXA_HUMAN	Q940F6 homo sapien
20	85.5	13.9	232	1 YBR2_YEAST	Q940F6 homo sapien
21	83.5	13.6	115	1 RNF6_HUMAN	Q940F6 homo sapien
22	83	13.5	685	1 ICP0_HSVB	Q940F6 homo sapien
23	82.5	13.4	532	1 ICP0_HSVB	Q940F6 homo sapien
24	80	13.0	284	1 GOLF_DROME	Q940F6 homo sapien
25	79.5	12.9	305	1 P48785_MOUSE	Q940F6 homo sapien
26	79.5	12.9	796	1 PRH_ARATH	Q940F6 homo sapien
27	79	12.8	381	1 RN13_CHICK	Q940F6 homo sapien
28	79	12.8	381	1 RN13_HUMAN	Q940F6 homo sapien
29	79	12.8	410	1 ICP0_PVIF	Q940F6 homo sapien
30	79	12.8	583	1 YOP7_SCHPO	Q940F6 homo sapien
31	79	12.8	1679	1 FUR2_DROME	Q940F6 homo sapien
32	78.5	12.7	235	1 YOF7_CAEL	Q940F6 homo sapien
33	78	12.7	381	1 RN13_MOUSE	Q940F6 homo sapien

34	77	12.5	279	1 SL13_HUMAN	Q14192 homo sapien
35	77	12.5	295	1 PEXA_PICAN	Q09340 picia angu
36	76.5	12.4	643	1 AMF2_HUMAN	Q940F6 homo sapien
37	76.5	12.4	643	1 AMF2_MOUSE	Q940F6 mus musculu
38	76.5	12.4	758	1 YK4_YEAST	P36096 saccharomyc
39	75	12.3	1493	1 M3K1_MOUSE	P53349 mus musculu
40	75	12.3	1493	1 M3K1_MOUSE	Q62825 rattus norv
41	76	12.3	1493	1 M3K1_HUMAN	Q13233 homo sapien
42	75.5	12.3	676	1 ICP0_HSVB	P29128 bovine herp
43	75.5	12.3	676	1 ICP0_HSVB	P29636 bovine herp
44	74.5	12.1	825	1 ICP0_HSV2H	P28284 herpes simp
45	74	12.0	474	1 CBLC_HUMAN	Q940F6 homo sapien

ALIGNMENTS

RESULT 1
ID RBX1_HUMAN STANDARD; PRT; 108 AA.
AC Q96268; Q9D1S2; Q9WUK3; Q9Y254;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1 (RDX1) (Regulator of cullin 1) (RING finger protein 75) (ZYP protein).
GN RBX1 OR ROCI OR RNF75.
OS Homo sapiens (Human), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606, 10090;
RN [1]
RP SEQUENCE FROM N.A., INTERACTION WITH CULLINS, AND MUTAGENESIS OF CY5-53; CY5-56; CY5-75 AND HIS-77.
RC SPECIES=Human; TISSUE=Cervical carcinoma;
RX MEDLINE=99247022; PubMed=10230407;
RA Ohta T., Michel J.J., Schottelius A.J., Xiong Y., "ROCI, a homolog of APC1, represents a family of cullin partners with an associated ubiquitin ligase activity.", Mol. Cell 3:535-541(1999).
RN [2]
RP SEQUENCE FROM N.A., AND IDENTIFICATION IN CBC(VHL) COMPLEX.
RC SPECIES=Human, and Mouse;
RX MEDLINE=99233320; PubMed=10233691;
RA Kanura T., Koepf D.M., Conrad M.N., Skowrya D., Moreland R.J., Iliopoulos O., Lane W.S., Kaelin W.G. Jr., Ellledge S.J., Conway R.C., Harper J.W., Conway J.W., "Rpx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase.", Science 284:657-661(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M., Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagshaw C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Buttrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conway D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Griffiths M.N.D., Hall C., Gilbert J.G.R., Goward M.B., Graham D.V., Griffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A., Laird G.K., Langford C.F., Leaverha M.A., Lloyd C., Lloyd D.M., Martin I.D., Mahegheh M., Mohammed M., Matthews L.H., McCann O.T., McElay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

Thu Mar 25 10:42:33 2004

us-09-914-324a-1.rsp

Query Match 100.0%; Score 616; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.5e-61;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMADVTPSGTNSGAGKRRFEVKKNVAVAMWDIVDNCALCRNHIMDLCEGCQANQ 60
DB 1 MAAMADVTPSGTNSGAGKRRFEVKKNVAVAMWDIVDNCALCRNHIMDLCEGCQANQ 60
QY 61 ASATSECTVAMGVGNHAFHFCISRMILKTRQVCPIDNREMEFQKXGH 108
DB 61 ASATSECTVAMGVGNHAFHFCISRMILKTRQVCPIDNREMEFQKXGH 108

RESULT 2
RBX1_SALSA STANDARD; PRT; 108 AA.

AC 08064:
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1 (Rbx1) (Hyperosmotic protein 21).
GN RBX1 OR SHOP21.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OC NCBI_TaxID=8030;
RX TISSUE=G11;
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION.
RC MEDLINE=22005592; PubMed=12010746;
RA Pan F., Zarate J., Bradley T.M.;
RT "A homolog of the E3 ubiquitin ligase Rbx1 is induced during
hyperosmotic stress of salmon."
RL Am. J. Physiol. 282:R1643-R1653(2002).
CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
ubiquitin ligase complex, which mediates the ubiquitination and
subsequent proteasomal degradation of target proteins. Through the
RING-type zinc finger, seems to recruit the E2 ubiquitination
enzyme, like CDC34, to the complex and brings it into close
proximity to the substrate (By similarity).
CC -1- PARTIAL: Ubiquitin conjugation; third step.
CC -1- SUBUNIT: Part of SCF complexes, which consist of SKP1, CUL1,
RBX1 and a F-box protein (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed in heart and kidney.
CC -1- INDUCTION: During hyperosmotic stress and thermal stress.
CC -1- DOMAIN: The RING-type zinc finger domain is essential for
ubiquitin ligase activity. It coordinates an additional third zinc
atom.
CC -1- SIMILARITY: Belongs to the RBX1 family.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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FT METAL 56 56 ZINC 3 (BY SIMILARITY).
FT METAL 68 68 ZINC 3 (BY SIMILARITY).
FT METAL 75 75 ZINC 2 (BY SIMILARITY).
FT METAL 77 77 ZINC 2 (BY SIMILARITY).
FT METAL 80 80 ZINC 1 (BY SIMILARITY).
FT METAL 82 82 ZINC 3 (BY SIMILARITY).
FT METAL 83 83 ZINC 1 (BY SIMILARITY).
FT METAL 94 94 ZINC 2 (BY SIMILARITY).
FT METAL 97 97 ZINC 2 (BY SIMILARITY).
SQ SEQUENCE 108 AA; 12318 MW; 44C3EA712CED7BB CR664;
Query Match 98.1%; Score 604; DB 1; Length 108;
Best Local Similarity 98.1%; Pred. No. 7.4e-60;
Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAMADVTPSGTNSGAGKRRFEVKKNVAVAMWDIVDNCALCRNHIMDLCEGCQANQ 60
DB 1 MAAMADVTPSGTNSGAGKRRFEVKKNVAVAMWDIVDNCALCRNHIMDLCEGCQANQ 60
QY 61 ASATSECTVAMGVGNHAFHFCISRMILKTRQVCPIDNREMEFQKXGH 108
DB 61 ASATSECTVAMGVGNHAFHFCISRMILKTRQVCPIDNREMEFQKXGH 108

RESULT 3

RBXA_DROME STANDARD; PRT; 108 AA.

AC 09W5EL; 077429;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1A (Regulator of cullins 1a) (drbx1).
GN ROCI1A OR CG16982 OR EG.115C2.11.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RX TISSUE=G11;
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Berns P.V., Betman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Butler K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.O., Hernandez J.R., Houck J.,
Houston D., Houston K.A., Howland T.J., Wei M.-H., Idagham C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison U.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
Palazzo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
Svitskys R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

CC ubiquitin ligase activity. It coordinates an additional zinc
atom (By similarity).
CC - SIMILARITY: Belongs to the RING-box family.
CC - SIMILARITY: Contains 1 RING-type zinc finger.
CC - CAUTION: Ref.2 sequence differs from that shown due to erroneous
gene model prediction.

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DR EMBL; AE003418; AAFA5536.1; ALT SEQ.
DR EMBL; AL031561; CAA20886.1; -.
DR PIR; T13388; T13388.
DR FLYBASE; FBgn0025638; Roco1a.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zfc-C3HC4_1.
KW PROSITE; PS50089; ZE_RING_2, 1.
KW Ub1 conjugation pathway; Nuclear protein; Developmental protein; Zinc;
KW Zinc-finger; Metal-binding.
FT ZN FING 53 98
FT DOMAIN 15 98
FT METAL 42 42 POLY-SER.
FT METAL 45 42 ZINC 1 (BY SIMILARITY).
FT METAL 53 42 ZINC 1 (BY SIMILARITY).
FT METAL 56 53 ZINC 3 (BY SIMILARITY).
FT METAL 68 56 ZINC 3 (BY SIMILARITY).
FT METAL 75 68 ZINC 3 (BY SIMILARITY).
FT METAL 77 77 ZINC 2 (BY SIMILARITY).
FT METAL 80 80 ZINC 2 (BY SIMILARITY).
FT METAL 82 82 ZINC 1 (BY SIMILARITY).
FT METAL 83 83 ZINC 3 (BY SIMILARITY).
FT METAL 94 83 ZINC 1 (BY SIMILARITY).
FT METAL 97 94 ZINC 2 (BY SIMILARITY).
FT MUTAGEN 59 59 ZINC 2 (BY SIMILARITY).
FT WITH R-68.
FT N->C LOSS OF FUNCTION WHEN ASSOCIATED
FT C->R LOSS OF FUNCTION WHEN ASSOCIATED
FT MUTAGEN 68 68 WITH C-59.
FT FT WITH C-59.

SQ SEQUENCE 108 AA; 12538 MW; 15784198281BCD13 CRC64;

Query Match 86.7%; Score 534; DB 1; Length 108;
Best Local Similarity 87.2%; Pred. No. 3.9e-52;
Matches 95; Conservative 4; Mismatches 4; Indels 6; Gaps 2

Dy 5 MDVD-----TSQTSGAGAKRFKFKNNNAVALWMDIVDNCAICRNHIMDLCTEQAN 59
| | | : | : |
Dy 1 MEVDDGYEVSSSKG-DXKRFVKNNNAVALWMDIVDNCAICRNHIMDLCTEQAN 59
| | | : | : |

Dy 60 QASATSECTVAWGVCNAPFHPCISRLTKRVCPPLNREPEPKYGH 108
| | | : | : |
Dy 60 QASATSECTVAWGVCNAPFHPCISRLTKRVCPPLNREPEPKYGH 108
| | | : | : |

Dy 60 QASATSECTVAWGVCNAPFHPCISRLTKRVCPPLNREPEPKYGH 108
| | | : | : |

DB 60 QASATSECTVAWGVCNAPFHPCISRLTKRVCPPLNREPEPKYGH 108
| | | : | : |

RESULT 4
REXA_ARATH STANDARD; PRT; 118 AA.
ID REXA_ARATH
AC Q94OX7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1a (RBX1A-Ac) (At-Rbx1.1) (RBX1-2).
GN RBX1A OR ARS30570 OR F7C8.160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]

FT METAL 104 104 ZINC 2 (BY SIMILARITY).
 FT METAL 107 107 ZINC 2 (BY SIMILARITY).
 SO SEQUENCE 118 AA; 13238 MW; 15947BF06F442A2 CRC64;
 Query Match 83.5%; Score 514.5; DB 1; Length 118;
 Best Local Similarity 78.6%; Pred. No. 6.1e-50;
 Matches 92; Conservative 6; Mismatches 8; Indels 11; Gaps 2;

QY 3 AAMVDVT---PSG-----TNSGAGKPEVKKNVAALMAMDIYVNCALICRNHND 51
 DB 2 ATLDSDVTMIRAGASSSVVAASNNKAKREIRKMSAVALLMAMDIYVNCALICRNHND 61
 QY 52 LCIECOANQASATSEECTVANGVCNHAFFHCISRMKTRQVCPDNDREWEFOKIGH 108
 DB 62 LCIECOANQASATSEECTVANGVCNHAFFHCISRMKTRQVCPDNDREWEFOKIGH 118

RESULT 5

RXB_X_ARATH STANDARD; PRT; 115 AA.

AC Q9M2B0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Putative RING-box protein 1b (RBX1b-Ac) (At-Rbx1.2) (RBX1-1).
 GN RBX1B OR AT3G42830 OR T21C14.50.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RX SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger H., Perez-Alonso M., Obermaier B.,
 RA Fatmann B., Valle G., Bloeker H., Macho R., Pulgomech P.,
 RA Delaney M., Boutry M., Griwall L.A., Mahe R., C. Brothier P.,
 RA De Simone V., Choisme N., Artiguenave F., Robert C., Brothier P.,
 RA Winkler P., Catolico L., Weisenbach U., Saurin W., Queirer F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Beres S.,
 RA Wurmbach E., Drzonek H., Exfle H., Jordan N., Bangert V.,
 RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
 RA Reinhardt U., Schaefer M., Schoen O., Bagnies M., Terol J., Clement J.,
 RA Navarro P., Colledo C., Perez-Perez A., Oltensweiler B., Duchemin D.,
 RA Cooke R., Laude M., Berger-Liauz J.-P., Cottet A.E., Casacuberta E.,
 RA de Haan M., Maere A.C., Alcaraz J.-P., Cottet A.E., Casacuberta E.,
 RA Montfort A., Argitrou A., Flores M., Liguori R., Vitale D.,
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pail G., Miltscher U., Sellers P., Gill J.Z., Feldlym T.V.,
 RA Prens D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Frazer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idegawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa S., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Matsuabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:820-822 (2000).

RN DISCUSSION OF SEQUENCE.
 RP MEDLINE=2204438; PubMed=12215511;
 RX Gray W.M., Hellmann H., Dharmasiri S., Estelle M.;
 RT "Role of the Arabidopsis RING-H2 protein RBX1 in RUB modification and
 SCF function.";
 RL Plant Cell 14:2137-2144 (2002).
 RN TISSUE SPECIFICITY.
 RP

RA MEDLINE=22370998; PubMed=12381738;
 RA Lechner E., Xie D., Grava S., Pigaglio E., Planchais S., Shen W.-H.,
 RA Murray J.A.H., Parmentier Y., Mutterer J., Dubreucq B., Shen W.-H.,
 RA Genschik P.;
 RT "The AtRbx1 protein is part of plant SCF complexes, and its
 down-regulation causes severe growth and developmental defects.";
 RL J. Biol. Chem. 277:50069-50080 (2002).

-1- FUNCTION: Potential component of the SCF (SKP1-CUL1-F-box protein)
 E3 ubiquitin ligase complex, which mediates the ubiquitination and
 subsequent proteasomal degradation of target proteins. The SCF
 complex plays a crucial role in regulating response to auxin and
 is essential for growth and development. Through the RING-type
 zinc finger, seems to recruit the E2 ubiquitination enzyme, to the
 complex and brings it into close proximity to the substrate (By
 similarity).
 CC SUBUNIT: Ubiquitin conjugation: third step.
 CC -1- SUBUNIT: Potential part of SCF complexes, which consist of a SKP1-
 related protein, a cullin, a RBX protein and a F-box protein.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Not detected in floral buds, stems and roots.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 ubiquitin ligase activity. It coordinates an additional third zinc
 atom.
 CC -1- SIMILARITY: Belongs to the RBX1 family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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 or send an email to license@sdb.ch).

DR EMBL, AT138639; CAB87200.1; -
 DR PIR, T47341; T47341.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART, SM00184; RING; 1.
 DR PROSITE, PS50089; ZF_RING_2; 1.
 KW Hypothetical protein; Ub1 conjugation pathway; Nuclear protein; Zinc;
 KW Zinc-finger; Metal-binding.

FT ZN_FING 60 107
 FT METAL 49 49 RING-TYPE.
 FT METAL 52 52 ZINC 1 (BY SIMILARITY).
 FT METAL 60 60 ZINC 3 (BY SIMILARITY).
 FT METAL 63 63 ZINC 3 (BY SIMILARITY).
 FT METAL 75 75 ZINC 3 (BY SIMILARITY).
 FT METAL 82 82 ZINC 2 (BY SIMILARITY).
 FT METAL 84 84 ZINC 2 (BY SIMILARITY).
 FT METAL 87 87 ZINC 1 (BY SIMILARITY).
 FT METAL 89 89 ZINC 3 (BY SIMILARITY).
 FT METAL 90 90 ZINC 1 (BY SIMILARITY).
 FT METAL 101 101 ZINC 2 (BY SIMILARITY).
 FT METAL 104 104 ZINC 2 (BY SIMILARITY).
 SO SEQUENCE 115 AA; 12999 MW; 1515E3B417DB1FAF CRC64;

QY Query Match 81.0%; Score 499; DB 1; Length 115;
 Best Local Similarity 81.5%; Pred. No. 3e-48;
 Matches 89; Conservative 5; Mismatches 13; Indels 2; Gaps 1;

DB 10 MGSSSSISVPS--SSSKNSRPFELKMSAVALLMAMDIYVNCALICRNHNDICIECLANO 67
 QY 61 ASATSEECTVANGVCNHAFFHCISRMKTRQVCPDNDREWEFOKIGH 108

DB 68 ASATSEECTVANGVCNHAFFHCISRMKTRQVCPDNDREWEFOKIGH 115

RESULT 6

RXB1_CABEL STANDARD; PRT; 110 AA.

Thu Mar 25 10:42:33 2004

us-09-914-324a-1.rsp

Page 7

AC Q23457; Q8WSQ1; 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE RING-box protein 1 (Rbx1) (Ce-rbx-1).
 GN RBX-1 OR ZK287.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Telodermata; Caenorhabditis.
 OK NCBI_taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brictol N2;
 RA McMurry A.A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 2-110 FROM N.A.
 RA Sasagawa Y., Urano T., Kohara Y., Takahashi H., Higashitani A.;
 RT "Characterization of rbx1 gene from Caenorhabditis elegans."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 ubiquitin ligase complex, which mediates the ubiquitination and
 subsequent proteasomal degradation of target proteins. Through the
 RING-type zinc finger, seems to recruit the E2 ubiquitination
 enzyme to the complex and brings it into close proximity to the
 substrate (By similarity).
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of SCF complexes, which consist of a SKP1 or a SKP1-
 related protein, a cullin protein, and a F-box protein (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 ubiquitin ligase activity. It coordinates an additional third zinc
 atom.
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-10 is the initiator.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Z70757; CAA94801.1; -
 DR EMBL; AB07287; BAB83695.1; ALT_INTT.
 DR PIR; T27823; T27823.
 DR WormBep; ZK287.5; CE06614.
 DR InterPro; IPR001841; Znf_Ring.
 DR Pfam; PF00097; ZF-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PSS00089; ZF_RING_2; 1.
 KM Ub1 conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 KM Metal-binding.
 FT ZN RING 44 100 RING-TYPE.
 FT METAL 44 44 ZINC 1 (BY SIMILARITY).
 FT METAL 47 47 ZINC 3 (BY SIMILARITY).
 FT METAL 55 55 ZINC 3 (BY SIMILARITY).
 FT METAL 58 58 ZINC 3 (BY SIMILARITY).
 FT METAL 70 70 ZINC 2 (BY SIMILARITY).
 FT METAL 77 77 ZINC 2 (BY SIMILARITY).
 FT METAL 79 79 ZINC 1 (BY SIMILARITY).
 FT METAL 82 82 ZINC 3 (BY SIMILARITY).
 FT METAL 84 84 ZINC 1 (BY SIMILARITY).
 FT METAL 85 85 ZINC 2 (BY SIMILARITY).
 FT METAL 96 96 ZINC 2 (BY SIMILARITY).
 FT METAL 99 99 ZINC 2 (BY SIMILARITY).
 FT CONFLICT 2 3 AQ -> GP (IN REF. 2).
 SQ SEQUENCE 110 AA; 12760 MW; EFES0F7664B30A56 CRC64;

Query Match 80.0%; Score 493; DB 1; Length 110;

Best Local Similarity 79.3%; Pred. No. 1.3e-47;
 Matches 88; Conservative 5; Mismatches 14; Indels 4; Gaps 2;
 QY 1 MAAMP---VDTSNGNSAGKREFEVKMNVAMAMIVDNCAGNHIMDLCECO 57
 DB 1 MAQASSTAMEVEATNQTV-KRFEVKMSAVAMAMDIQVNCALCRNHIMDLCECO 59
 QY 58 ANQASATSECTVAMGVCMNAFFPHCISRLKTRQVCPDNRWEPQKXG 108
 DB 60 ANQAGKDECTVAMGNCHNAFFPHCISRLKTRQVCPDNRWEPQKXG 110
 RESULT 7
 RBX1 SCHPO STANDARD; PRT; 107 AA.
 AC 013959;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE RING-box protein p1p1 (Pop-interacting protein 1) (RING-box protein
 1).
 GN P1P1 OR SPAC23H4.18C.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OK NCBI_taxid=4896;
 RN [1]
 RP SEQUENCE FROM N.A.; FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION
 WITH POP1, POP2 AND PCUL1.
 RX MEDLINE=22325333; PubMed=2167173;
 RA Seibert V., Prohl C., Schultze I., Rhee E., Lopez R., Abderazzag K.,
 RA Zhou C., Wolf D.A.;
 RT "Combinatorial diversity of fission yeast SCF ubiquitin ligases by
 RT home- and heterooligomeric assemblies of the F-box proteins Pop1p and
 RT Pop2p."
 RL BMC Biochem. 3:22-22 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=2184940; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream K.A., Lyne M., Lyne R., Stewart A.,
 RA Squares J., Peat N., Hayles D., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Falwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Wungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
 RA Wellens I., Vansteelandt E., Rieger M., Schneider M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinich H., Reinhardt J., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
 RA Goffeau A., Cadieu A., Dreano S., Gloux S., Lelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Ulmenz J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen O., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880 (2002).
 CC -1- FUNCTION: Component of E3 ubiquitin ligase SCF complexes, which
 mediate the ubiquitination and subsequent proteasomal degradation
 of target proteins. Seems to recruit the E2 ubiquitination enzyme,
 like UBC3/CDC34, to the complex and brings it into close proximity
 to the substrate.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.

CC -1- SUBUNIT: Part of a SCF E3 ubiquitin ligase complex containing
 CC psh1, pip1, pull1 and the F-box proteins pop1 and pop2. Instead of
 CC the pop1/pop2 heterodimer also homooligomers of pop1 or pop2 may
 CC be present in the complex.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC -----
 CC DR EMBL; AF192228; AAD54393.1; -
 CC DR PIR; T38310; T38310.
 CC DR GeneDB; Spombe; SPAC23H4.18c; -
 CC DR InterPro; IPR001841; Znf_fing.
 CC DR Pfam; PF00097; Zf-C3HC4; 1.
 CC DR SMART; SM00184; RING; 1.
 CC DR PROSITE; PS50089; ZF_RING_2; 1.
 CC KM ubi conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 KM Metal-binding.
 FT ZN FING 52 97 RING-TYPE.
 FT METAL 41 41 ZINC 1 (BY SIMILARITY).
 FT METAL 44 44 ZINC 3 (BY SIMILARITY).
 FT METAL 52 52 ZINC 1 (BY SIMILARITY).
 FT METAL 55 55 ZINC 3 (BY SIMILARITY).
 FT METAL 67 67 ZINC 3 (BY SIMILARITY).
 FT METAL 74 74 ZINC 2 (BY SIMILARITY).
 FT METAL 76 76 ZINC 2 (BY SIMILARITY).
 FT METAL 79 79 ZINC 1 (BY SIMILARITY).
 FT METAL 81 81 ZINC 3 (BY SIMILARITY).
 FT METAL 82 82 ZINC 1 (BY SIMILARITY).
 FT METAL 93 93 ZINC 2 (BY SIMILARITY).
 FT METAL 96 96 ZINC 2 (BY SIMILARITY).
 SQ SEQUENCE 107 AA; 12724 MW; 71C3A3D2BF26DABF CRC64;
 Query Match 76.1%; Score 469; DB 1; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.8e-45;
 Matches 77; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 21 REVEKKNVAVLWADIYVNCALCRNIMDLCEQANQASATSECTVAMGVGNHAFH 80
 DB 20 REIRKKNVAVLWMDIVDNCALGRNIMDLCEQANTSAQAQETVAMGVGNHAFH 79
 QY 81 FHGISRWLKTQVCPIDNREWFQYKH 108
 DB 80 FHGISRWLKTQVCPIDNREWFQYKH 107
 RESULT 8
 REB: DROME STANDARD; PRT; 122 AA.
 ID RBXB DROME
 AC Q9NHX0; Q9W0R1;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein 1b (Regulator of cullins 1b).
 GN RING-box protein 1b (Regulator of cullins 1b).
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION AND TISSUE SPECIFICITY.
 RX MEDLINE=22057626; PubMed=12062088;

RA Nouredine M.A., Donaldson T.D., Thacker S.A., Duronio R.D.;
 RT "Drosophila Roca encodes a RING-H2 protein with a unique function in
 RT processing the Hb signal transducer Ci by the SCF E3 ubiquitin
 RT ligase.";
 RL Dev. Cell 2:757-770(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blake J.R., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bandaru D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Boulton P., Brothier P.,
 RA Burris K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos J.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.U., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison U.A., Kechum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei J.B., McIntosh T.C., McLeod M.P., McPherson J.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M., M.G.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.F., Zaveri J.S., Zhao W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zheng X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=Testis;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Garin H., Krommiller B., Paclet J.M., Park S., Wan K.H.,
 RA Rubin G.M., Gelniker S.E.;
 RT "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC ubiquitin ligase complex, which mediates the ubiquitination and
 CC subsequent proteasomal degradation of target proteins. Through the
 CC RING-type zinc finger, seems to recruit the E2 ubiquitination
 CC enzyme to the complex and brings it into close proximity to the
 CC substrate (By similarity).
 CC -1- SUBUNIT: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of a SCF complex consisting of Skp1 (SKP1),
 CC Ltn1 (CUL1), Roc1b and a F-box protein (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highly expressed in early embryos, and in
 CC pupae. Widely expressed in adult males, while it is weakly
 CC expressed in adult females.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom (By similarity).
 CC -1- SIMILARITY: Belongs to the RING-box family.

CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-16 is the initiator.
 CC -----
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 CC EMBL: AF218299; AAF32313.1; ALT_INIT.
 CC EMBL: AE003468; AAF47382.1; -.
 CC EMBL: AY070810; AAL48432.1; -.
 CC FLYBASE: FBgn0040291; Rocl.b.
 CC InterPro: IPR001841; Znf_ring.
 CC Pfam: PF000097; zf-C3HC4; 1.
 CC SMART: SM00184; RING; 1.
 CC PROSITE: PS50089; ZF_RING_2; 1.
 CC Ubl conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 CC Metal-binding.
 CC FT ZN FING 57 112 RING-TYPE.
 CC FT METAL 68 68 ZINC 3 (BY SIMILARITY).
 CC FT METAL 71 71 ZINC 3 (BY SIMILARITY).
 CC FT METAL 82 82 ZINC 3 (BY SIMILARITY).
 CC FT METAL 96 96 ZINC 3 (BY SIMILARITY).
 CC FT METAL 57 57 ZINC 1 (BY SIMILARITY).
 CC FT METAL 60 60 ZINC 1 (BY SIMILARITY).
 CC FT METAL 89 89 ZINC 2 (BY SIMILARITY).
 CC FT METAL 91 91 ZINC 2 (BY SIMILARITY).
 CC FT METAL 94 94 ZINC 1 (BY SIMILARITY).
 CC FT METAL 97 97 ZINC 1 (BY SIMILARITY).
 CC FT METAL 108 108 ZINC 2 (BY SIMILARITY).
 CC FT METAL 111 111 ZINC 2 (BY SIMILARITY).
 CC SQ SEQUENCE 122 AA; 14225 MW; F22CE00438725410 CR664;
 CC
 CC Query Match 65.0%; Score 400.5; DB 1; Length 122;
 CC Best Local Similarity 65.4%; Pred. No. 2.4e-37;
 CC Matches 70; Conservative 13; Mismatches 19; Indels 5; Gaps 2;
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 CC QY 5 MVDTPSGNSG---AGKREYKKNVAALAMADIVDNCAIRNIMDLCECOAQ 60
 CC DB 16 MGFNEBPSCGAVQARTERFVKKVAHAWMGVDVAADNCAIRNIMDLCECOAD 74
 CC QY 61 ASATSECTVANGVCHAFPHICISRWLKTROVCEPLDNREMEFOKYG 107
 CC DB 75 PRANODECTVANGCHAFPHICIAWLTIRLVCPDLNKEWYQKYG 121
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 CC RESULT 9
 CC RBX1 YEAST STANDARD; PRT; 121 AA.
 CC ID RBX1 YEAST 008273;
 CC AC 10-OCT-2003 (Rel. 42, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC DE RING-box protein HRT1 (RING-box protein 1).
 CC GN HRT1 OR RBX1 OR YOL133W.
 CC OS Saccharomyces cerevisiae (Baker's Yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CC NCBI_TaxId=4932;
 CC RN NCB1_TaxId=4932;
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=8288C / FY1679;
 CC RX MEDLINE=97051593; PubMed=8896270;
 CC RA Aldela M., Piedrafilta L., Casas C., Casamayor A., Khalid H.,
 CC Balcells L., Arino J., Herrero B.;
 CC "Sequence analysis of a 12 801 bp fragment of the left arm of yeast
 CC chromosome XV containing a putative 6-phosphofructo-2-kinase gene, a
 CC RT gene for a possible glycopospholipid-anchored surface protein and
 CC RT six other open reading frames."
 CC RT Yeast 12:1053-1058(1996).
 CC RL

EN [2]
 RP SEQUENCE OF 8-31, FUNCTION, INTERACTION WITH CDC53, CDC4 AND
 RP CDC34, AND IDENTIFICATION IN SCF COMPLEX.
 RX MEDLINE=99315634; PubMed=10385629;
 RA Seol J.H., Feldman R.M.R., Zachariae W., Shevchenko A., Correll C.C.,
 RA Iyavarna S., Chi Y., Galova M., Claypool J., Sandmeyer S., Naemlyth K.,
 RA Shevchenko A., Deshaies R.J.;
 RT Cdc3/cullin and the essential Hrt1 RING-H2 subunit of SCF define a
 RT ubiquitin ligase module that activates the E2 enzyme Cdc34.";
 RT Genes Dev. 13:1614-1626(1999).
 RN [3]
 RP IDENTIFICATION IN SCF COMPLEX, INTERACTION WITH CDC34 AND CDC4, AND
 RP MUTANT RBX1-1.
 RX MEDLINE=99234321; PubMed=10213692;
 RA Skowra D., Koepf D.M., Kamura T., Conrad M.N., Conaway R.C.,
 RA Conaway U.W., Elledge S.J., Harper J.W.;
 RT "Reconstitution of G1 cyclin ubiquitination with complexes containing
 RT SCFGrl and Rbx1.";
 RT Science 284:662-665(1999).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=20047893; PubMed=10579999;
 RA Kamura T., Conrad M.N., Yan Q., Conaway R.C., Conaway U.W.;
 RT "The Rbx1 subunit of SCF and VHL E3 ubiquitin ligase activates Rbx1
 RT modification of cullins Cdc53 and Cul2.";
 RL Genes Dev. 13:2928-2933(1999).
 RN [5]
 RP SUBCELLULAR LOCATION AND MUTANT HRT1-C81Y.
 RX MEDLINE=20341308; PubMed=10880467;
 RA Blondel M., Galan U.-W., Peter M.;
 RT "Isolation and characterization of Hrt1 using a genetic screen for
 RT mutants unable to degrade Gic2p in Saccharomyces cerevisiae.";
 RL Genetics 155:1033-1044(2000).
 CC -1- FUNCTION: Component of E3 ubiquitin ligase SCF complexes, which
 CC mediate the ubiquitination and subsequent proteasomal degradation
 CC of target proteins. Seems to recruit the E2 ubiquitination enzyme,
 CC like UBC3/CDC4, to the complex and brings it into close proximity
 CC to the substrate. Also stimulates UBC3/CDC34 autoubiquitination
 CC and promotes the neddylation of CDC53.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of SCF E3 ubiquitin ligase complexes containing
 CC CBF3, CDC53, HRT1 and F-box proteins YUL149W or GR1. Interacts
 CC with CDC53, CDC4 and UBC3.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity.
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
 CC -----
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 CC -----
 CC EMBL: X93465; CA64737.1; -.
 CC EMBL: Z74876; CA93155.1; -.
 CC PIR: S66830; S66830.
 CC SGD: S0005493; HRT1.
 CC GO: GO:0005737; C:cytoplasm; IDA.
 CC GO: GO:0005634; C:nucleus; IDA.
 CC GO: GO:0005315; F:protein binding; IPI.
 CC GO: GO:0004842; F:ubiquitin-protein ligase activity; IDA.
 CC InterPro: IPR001841; Znf_ring.
 CC SMART: SM00184; RING; 1.
 CC PROSITE: PS50089; ZF_RING_2; 1.
 CC Ubl conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 CC Metal-binding.
 CC FT ZN FING 55 111 RING-TYPE.
 CC FT METAL 55 55 ZINC 1 (BY SIMILARITY).
 CC FT

RA Klausner R.U., Collins J.S., Wagner L., Schenken C.M., Schaefer G.C., Bhat N.K.,
 Ralschul S.F., Ziegler B., Buettner R., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McWay P.J., McKernan K.J., Nalek J.A., Gunaratne P.H.,
 RA Richards S., Coleman K.C., Hale S., Garcia A.M., Gay L.W., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." ,
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RP IDENTIFICATION IN APC/C COMPLEX.
 RX MEDLINE=903813321; PubMed=10922056;
 RA Gmachl M., Gieffers C., Podtelejnikov A.V., Mann M., Peters J.-M.;
 RT "The RING-H2 finger protein APC1 and the E2 enzyme UBC4 are
 RT sufficient to ubiquitinate substrates of the anaphase-promoting
 RT complex." ,
 Proc. Natl. Acad. Sci. U.S.A. 97:8973-8978(2000).
 [6]
 RP FUNCTION, MUTAGENESIS, AND INTERACTION WITH ANAPC2 AND UBE2D2.
 RX MEDLINE=21602823; PubMed=11739784;
 RA Tang Z., Li B., Bhargadwaj R., Zhu H., Ozekkan E., Hakala K.,
 RA Deisenhofer J., Yu H.;
 RA "APC2: cullin protein and APC1 RING protein comprise the minimal
 RT ubiquitin ligase module of the anaphase-promoting complex." ,
 Mol. Biol. Cell 12:3839-3851(2001).
 CC -1- FUNCTION: Component of the anaphase promoting complex/cytosome
 CC (APC/C), a cell cycle-regulated E3 ubiquitin ligase that controls
 CC progression through mitosis and the G1 phase of the cell cycle.
 CC May recruit the E2 ubiquitin-conjugating enzymes to the complex.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: The APC/C is composed of at least 11 subunits. Interacts
 CC with the cullin domain of ANAPC2. Interacts with UBE2D2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9NTG5-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9NTG5-2; Sequence=VSP_008450;
 CC Note=Non experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Expressed at high levels in skeletal muscle
 CC and heart; in moderate levels in brain, kidney, and liver; and at
 CC low levels in colon, thymus, spleen, small intestine, placenta,
 CC lung and peripheral blood leukocyte.
 CC -1- DOMAIN: The RING-type zinc finger domain coordinates an additional
 CC third zinc atom.
 CC -1- PTM: Auto-ubiquitylated.
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 67.
 CC
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 CC EMBL, AF247565; AAF65816.1; -
 CC EMBL, AF247789; AAL95694.1; -
 CC EMBL, AF151048; AAF36134.1; ALT_FRAME.

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DR EMBL; BC000607; AAH00607.1; -
DR Genew; HGNC; 14452; ANAPC11.
DR GK; OGNYS; -
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING_1; Znf_ring.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Ubl conjugation pathway; Cell cycle; Cell division; Mitosis; Zinc;
KW Zinc-finger; Metal-binding; Nuclear protein; Ubl conjugation;
KW Alternative splicing.
FT ZN FING 34 77 RING-TYPE.
FT METAL 23 23 ZINC 1 (BY SIMILARITY).
FT METAL 26 26 ZINC 1 (BY SIMILARITY).
FT METAL 34 34 ZINC 3 (BY SIMILARITY).
FT METAL 37 37 ZINC 3 (BY SIMILARITY).
FT METAL 44 44 ZINC 3 (BY SIMILARITY).
FT METAL 51 51 ZINC 2 (BY SIMILARITY).
FT METAL 53 53 ZINC 2 (BY SIMILARITY).
FT METAL 56 56 ZINC 2 (BY SIMILARITY).
FT METAL 58 58 ZINC 3 (BY SIMILARITY).
FT METAL 59 59 ZINC 1 (BY SIMILARITY).
FT METAL 73 73 ZINC 2 (BY SIMILARITY).
FT METAL 76 76 ZINC 2 (BY SIMILARITY).
FT VARSPLIC 1 37 MKVKIKCMGVATLWLVANDENCGICRMAFNGCCPDC ->
/Flid=VSP_008450.
FT MUTAGEN 23 23 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 26 26 ACTIVITY.
FT MUTAGEN 34 34 C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 37 37 C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 44 44 C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 51 51 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 53 53 H->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 56 56 ACTIVITY.
FT MUTAGEN 58 58 H->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 59 59 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 73 73 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 76 76 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT SEQUENCE 84 AA; 9841 MW; EACGBSAS4FCDC11AE CRC64;
SQ
Query Match 33.8%; Score 208; DB 1; Length 84;
Best Local Similarity 37.5%; Pred. No. 2.8e-16;
Matches 33; Conservative 17; Mismatches 30; Indels 8; Gaps 2;

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OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;
RN
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RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=2184901; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagers K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymopoulos B.,
RA Melchens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moesli D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Polt T.M.,
RA Eger P., Zimmermann W., Medler H., Wambutt R., Furnelle B.,
RA Goffeau A., Cadieu E., Diano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Rhode G.,
RA Dama R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
RN
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshida S., Kato K., Nakai K., Okayama H., Nojima H.,
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNA."
RL DNA Res. 4:363-369(1997).
CC
-1- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC
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DR EMBL; AL109739; CAB52266.1; -
DR EMBL; AB001022; BA19216.1; ALT_SEQ.
DR PIR; T38652; T38652.
DR GeneDB Spombe; SPAC343.03; -
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING_1;
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Zinc-finger.
FT ZN FING 35 78 RING-TYPE.
FT SEQUENCE 94 AA; 10557 MW; C770021339C3626 CRC64;
SQ
Query Match 26.7%; Score 164.5; DB 1; Length 94;
Best Local Similarity 33.7%; Pred. No. 2e-11;
Matches 28; Conservative 16; Mismatches 30; Indels 9; Gaps 3;

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QY 80 HFFHCISRWLKT---ROYCPDNR 99
 DB 57 HAHCIQWNLATSGSQGCPYDRQ 79

RESULT 15

RN24_HUMAN STANDARD; PRT; 148 AA.

AC Q9Y225; Q9YH01; Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE RING finger protein 24.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 OX [1]

RP SEQUENCE FROM N.A. PubMed=11780052;
 RX MEDLINE=21638749;

RA DeJours F., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark R.E., Connor R.E., Corby N.R.,
 RA Clegg S., Cobley V.E., Collier R.E., Dhami P.D., Dunn M.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Gillingham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaerajaho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McKernson T.,
 RA Milne S.A., Misty D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Trzeman A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).

RN [2]
 RP SBOUENCE FROM N.A.
 RX TISSUE=Blood, and kidney;
 RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherach A., Schein J.E., Jones S.J.M., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]

RP SEQUENCE OF 45-148 FROM N.A.
 RA Basal M.T., Banfi S., Raboni M., Ballabio A., Boreani G.,
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC -----
 DR EMBL, AL096778; CAB46627.1; -
 DR EMBL, AL031670; CAB43182.1; -
 DR EMBL, BC000213; AAH00213.1; -
 DR EMBL, BC039584; AAH39584.1; -
 DR EMBL, AL079313; CAB45279.1; -
 DR HSSP, P28990; ICRC.
 DR Genew; HGNC:13779; RNF24.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; ZF-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00589; ZF_RING_2; 1.
 KW Zinc-finger.
 FT ZN-FING 78 119 RING-TYPE.
 FT ZN-CONFICT 45 45 Y->S (IN REF. 3).
 SO SEQUENCE 148 AA; 17209 MW; 66C240C3A5991EAS CRC64;

QY 75 CNAHFFHCISRWLKTROYCPDNR 98
 DB 96 CKHAFKRLKXWLEVKYCPDNR 119
 Search completed: March 25, 2004, 09:35:15
 Job time: 17 secs
 Query Match 14.8%; Score 91; DB 1; Length 148;
 Best Local Similarity 58.3%; Pred. No. 0.0041;
 Matches 14; Conservative 4; Indels 0; Gaps 0;

Thu Mar 25 10:42:33 2004

us-09-914-324a-1.rapb

Page 1

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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:36:13 / Search time 41 Seconds

(without alignments)
689,255 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMVDVTPSGTNSGAGKK.....KTRQVCPDNRMEFQKXGH 108

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1065169 seqs, 26161801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	616	100.0	108	9	US-09-826-312-6
2	616	100.0	108	14	US-10-108-767-6
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4	518.5	84.2	118	12	US-10-424-599-148916
5	506.5	82.2	152	12	US-10-424-599-221431
6	420.5	68.3	106	12	US-10-424-599-148915
7	313	50.8	75	12	US-10-424-599-230014
8	292	47.4	118	9	US-09-764-864-826
9	292	47.4	131	9	US-09-764-864-1285
10	287	46.6	64	12	US-10-424-599-228320
11	287	46.6	113	9	US-09-826-312-8
12	287	46.6	113	14	US-10-108-767-8
13	287	46.6	113	14	US-10-152-156-8
14	282	45.8	68	12	US-10-424-599-242288
15	228	37.0	40	12	US-10-424-599-264079

16	213	34.6	88	12	US-10-276-774-2678	Sequence 2678, Ap
17	213	34.6	88	14	US-10-102-806-520	Sequence 620, App
18	213	34.6	91	15	US-10-264-049-2937	Sequence 2937, Ap
19	213	34.6	105	9	US-09-764-864-1274	Sequence 1274, Ap
20	210	34.1	124	9	US-09-764-864-1284	Sequence 1284, Ap
21	208	33.8	84	12	US-10-221-625-94	Sequence 94, Appl
22	208	33.8	100	12	US-10-424-599-253860	Sequence 253860, Ap
23	202	32.8	84	9	US-09-826-312-5	Sequence 5, Appl
24	202	32.8	84	14	US-10-108-767-5	Sequence 5, Appl
25	202	32.8	84	14	US-10-152-156-5	Sequence 5, Appl
26	196	31.8	85	15	US-10-264-049-2926	Sequence 2926, Ap
27	185.5	30.1	121	9	US-09-764-864-839	Sequence 839, App
28	185.5	30.1	121	9	US-09-764-864-1294	Sequence 1294, Ap
29	185.5	30.1	121	10	US-09-764-891-4639	Sequence 4639, Ap
30	175	28.4	73	12	US-10-424-599-235108	Sequence 235108, Ap
31	172	27.9	114	15	US-10-320-797-3003	Sequence 3003, Ap
32	138	22.4	34	12	US-10-424-599-254645	Sequence 254645, Ap
33	134.5	21.8	133	14	US-10-032-585-7259	Sequence 7259, Ap
34	102	16.6	144	12	US-10-424-599-279773	Sequence 279773, Ap
35	100.5	16.3	205	12	US-10-424-599-213911	Sequence 213911, Ap
36	98	15.9	234	12	US-10-424-599-266133	Sequence 266133, Ap
37	97.5	15.8	128	12	US-10-424-599-202979	Sequence 202979, Ap
38	97.5	15.8	195	12	US-10-425-114-16967	Sequence 16967, A
39	97.5	15.8	209	12	US-10-425-114-41999	Sequence 41999, A
40	97.5	15.8	209	12	US-10-425-114-63173	Sequence 63173, A
41	96.5	15.7	345	12	US-10-425-114-71489	Sequence 71489, A
42	96.5	15.7	356	12	US-10-424-599-179820	Sequence 179820, A
43	95.5	15.5	100	12	US-10-425-114-450203	Sequence 450203, A
44	95.5	15.5	202	12	US-10-424-599-254121	Sequence 254121, A
45	95.5	15.5	344	12	US-10-424-599-143394	Sequence 143394, A

ALIGNMENTS

RESULT 1
US-09-826-312-6
Sequence 6, Application US/09826312
Patent No. US20020042083A1
GENERAL INFORMATION:
APPLICANT: Iseakani, Sarkiz D.
APPLICANT: Huang, Jialie
APPLICANT: Sheung, Jialie
TITLE OF INVENTION: US/QUITTIN LIGASE ASSAY
FILE REFERENCE: A-68613-1/RMS/JCD
CURRENT APPLICATION NUMBER: US/09/826,312
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-312-6

Query Match 100.0% Score 616 DB 9 Length 108
Best Local Similarity 100.0% Pred. No. 1.2e-60
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 MAAMVDVTPSGTNSGAGKREVKNAVALMWDIVDNCALCRNHINDLCTEQANQ 60
Db 1 MAAMVDVTPSGTNSGAGKREVKNAVALMWDIVDNCALCRNHINDLCTEQANQ 60
QY 61 ASATSECTVAVGVNHAFFHFCISRMUKTROVCPDNRMEFQKXGH 108
Db 61 ASATSECTVAVGVNHAFFHFCISRMUKTROVCPDNRMEFQKXGH 108
RESULT 2
US-10-108-767-6

Sequence 6, Application US/10108767
Publication No. US2003010447A1
GENERAL INFORMATION:
APPLICANT: Issakani, Sarkiz D.
APPLICANT: Huang, Jiating
APPLICANT: Sheung, Julie
APPLICANT: Pray, Todd R.
TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
FILE REFERENCE: A-68613-5/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/108,767
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 09/826,312
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 10/091,139
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-767-6

Query Match 100.0%; Score 616; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMDVTPSGTSGAGKKEFEYKKNVAVLWMDIVDNCACRHHNDLCIECOAQ 60
DB 1 MAAMDVTPSGTSGAGKKEFEYKKNVAVLWMDIVDNCACRHHNDLCIECOAQ 60

QY 61 ASATSECTVAMGVGNHAFHFCISRWLKTROVCPDNRREWEFOKYGH 108
DB 61 ASATSECTVAMGVGNHAFHFCISRWLKTROVCPDNRREWEFOKYGH 108

RESULT 3
US-10-152-156-6
Sequence 6, Application US/10152156
Publication No. US20030108947A1
GENERAL INFORMATION:
APPLICANT: Issakani, Sarkiz D.
APPLICANT: Huang, Jiating
APPLICANT: Sheung, Julie
APPLICANT: Pray, Todd R.
TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
FILE REFERENCE: A-68613-6/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/152,156
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 09/826,312
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 10/091,174
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 10/091,139
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 10/109,460
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 10/108,767
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/291,836
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens

US-10-152-156-6

Query Match 100.0%; Score 616; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMDVTPSGTSGAGKKEFEYKKNVAVLWMDIVDNCACRHHNDLCIECOAQ 60
DB 1 MAAMDVTPSGTSGAGKKEFEYKKNVAVLWMDIVDNCACRHHNDLCIECOAQ 60

QY 61 ASATSECTVAMGVGNHAFHFCISRWLKTROVCPDNRREWEFOKYGH 108
DB 61 ASATSECTVAMGVGNHAFHFCISRWLKTROVCPDNRREWEFOKYGH 108

RESULT 4
US-10-424-599-148916
Sequence 148916, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 148916
LENGTH: 118
TYPE: PRT
ORGANISM: Glycine max

Query Match 84.2%; Score 518.5; DB 12; Length 118;
Best Local Similarity 80.3%; Pred. No. 9.1e-50;
Matches 94; Conservative 5; Mismatches 7; Indels 11; Gaps 3;

QY 3 AAMDVTPSGTSGAGKKEFEYKKNVAVLWMDIVDNCACRHHND 51
DB 2 ATLDSDVTVFPAEASSSSGPESSSTKKPRREIKKNVAVLWMDIVDNCACRHHND 61

QY 52 LCIECOANASATSECTVAMGVGNHAFHFCISRWLKTROVCPDNRREWEFOKYGH 108
DB 62 LCIECOANASATSECTVAMGVGNHAFHFCISRWLKTROVCPDNRREWEFOKYGH 118

RESULT 5
US-10-424-599-221431
Sequence 221431, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 221431
LENGTH: 152
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_41982C.1.pep
US-10-424-599-221431

Thu Mar 25 10:42:33 2004

us-09-914-324a-1.rapb

Page 3

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FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_49727C.1.pdp
US-10-424-599-230014
Query Match      82.2%; Score 506.5; DB 12; Length 152;
Best Local Similarity 80.0%; Pred. No. 2.5e-48;
Matches 92; Conservative 4; Mismatches 10; Indels 9; Gaps 2;

QY 3 AAMVDTP-----SGTNSGAG-----KKRFVKKNNAAVLAAMDIVDNCACRHHIMDL 53
DB 38 ATLSDVPMVPAAGESSAGPSSKKPKRFEIKKNNAAVLAAMDIVDNCACRHHIMDL 97

QY 54 IECQANQASATSECTVAMGVCHNAFHFCISRWLKTROVCPDLDNREMEFOKYGH 108
DB 98 IECQANQASATSECTVAMGVCHNAFHFCISRWLKTROVCPDLDNREMEFOKYGH 152

RESULT 6
US-10-424-599-148915
; Sequence 148915, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285864
; SEQ ID NO 148915
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)..(106)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105493C.1.pdp
US-10-424-599-148915
Query Match      68.3%; Score 420.5; DB 12; Length 106;
Best Local Similarity 69.2%; Pred. No. 6.1e-39;
Matches 81; Conservative 5; Mismatches 8; Indels 23; Gaps 4;

QY 3 AAMVDTP-----PSG-TNSGAG-----KKRFVKKNNAAVLAAMDIVDNCACRHHIMD 51
DB 2 ATLSDVPMVPAAGESSAGPSSSTKKPKRFEIKKNNAAVLAAMDIVDNCACRHHIMD 61

QY 52 LCTECQANQASATSECTVAMGVCHNAFHFCISRWLKTROVCPDLDNREMEFOKYGH 108
DB 62 LCTECQANQASATSECTVAM-----XRWLKTROVCPDLDNREMEFOKYGH 106

RESULT 7
US-10-424-599-230014
; Sequence 230014, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285864
; SEQ ID NO 230014
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
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FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_49727C.1.pdp
US-10-424-599-230014
Query Match      50.8%; Score 313; DB 12; Length 75;
Best Local Similarity 51.7%; Pred. No. 3.7e-27;
Matches 58; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 40 DN-CAICRHHIMDL-CIECQANQASATSECTVAMGVCHNAFHFCISRWLKTROVCPD 97
DB 5 DNLCSARHSHSGFSASECQANQASATSECTVAMGVCHNAFHFCISRWLKTROVCPD 64

QY 98 NREMEFOKYGH 108
DB 65 NSEMEFOKYGH 75

RESULT 8
US-09-764-864-826
; Sequence 826, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 826
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-826
Query Match      47.4%; Score 292; DB 9; Length 118;
Best Local Similarity 50.5%; Pred. No. 1.3e-24;
Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;

QY 11 SGTNSGAGKKRFVKKNNAAVLAAMDIVDNCACRHHIMDLCTECQANQASATSECTV 70
DB 25 SGSRKSG-GDKKFFSLKKNNAAVLAAMSWDECDTCACRQVMDACLRQDAEN---KQEDCVV 80

QY 71 AMGVCHNAFHFCISRWLKTROVCPDLDNREMEFOKYGH 107
DB 81 VMGECHNSFRNCCMSLWVKNNRCFLCQDDMVVQRI 117

RESULT 9
US-09-764-864-1285
; Sequence 1285, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1285
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1285
Query Match      47.4%; Score 292; DB 9; Length 131;
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Best Local Similarity 50.5%; Pred. No. 1,4e-24;
Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;

QY 11 SGTNSGAGKRFYKKNVAVLWAMDIVDNCALICGNHIMDLCEQANQASATSECTV 70
DB 38 SGTSG-GDKMFSLKKNVAVLWAMDIVDNCALICGNHIMDLCEQANQASATSECTV 93
QY 71 AMGCNHAFFHCISRMLKTRQVCPDLNREWEFOKYG 107
DB 94 VMGCNHSFHNCCMSLWVKQNNRCPLCQGDWVVOIG 130

RESULT 10

US-10-424-599-238320
; Sequence 238320, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 238320
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_57228C.1.pep
US-10-424-599-238320

Query Match 46.6%; Score 287; DB 12; Length 64;
Best Local Similarity 77.8%; Pred. No. 2,4e-24;
Matches 49; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 45 CRNIMDLCEQANQASATSECTVAMGCNHAFFHCISRMLKTRQVCPDLNREWEFO 104
DB 1 CRNIMDLCEQANQASATSECTVAMGCNHAFFHCISRMLKTRQVCPDLNREWEFO 60
QY 105 KYG 107
DB 61 KYG 63

RESULT 11

US-09-826-312-8
; Sequence 8, Application US/09826312
; Patent No. US20020042083A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
; FILE REFERENCE: A-68613-1/RMS/JUD
; CURRENT APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-312-8

Query Match 46.6%; Score 287; DB 9; Length 113;
Best Local Similarity 49.5%; Pred. No. 4,3e-24;

Matches 48; Conservative 14; Mismatches 31; Indels 4; Gaps 2;

QY 11 SGTNSGAGKRFYKKNVAVLWAMDIVDNCALICGNHIMDLCEQANQASATSECTV 70
DB 20 SGTSG-GDKMFSLKKNVAVLWAMDIVDNCALICGNHIMDLCEQANQASATSECTV 75
QY 71 AMGCNHAFFHCISRMLKTRQVCPDLNREWEFOKYG 107
DB 76 VMGCNHSFHNCCMSLWVKQNNRCPLCQGDWVVOIG 112

RESULT 12

US-10-108-767-8
; Sequence 8, Application US/10108767
; Publication No. US20030104474A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGEN
; TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
; FILE REFERENCE: A-68613-5/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/108,767
; PRIOR FILING DATE: 2002-09-26
; CURRENT APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-767-8

Query Match 46.6%; Score 287; DB 14; Length 113;
Best Local Similarity 49.5%; Pred. No. 4,3e-24;
Matches 48; Conservative 14; Mismatches 31; Indels 4; Gaps 2;

QY 11 SGTNSGAGKRFYKKNVAVLWAMDIVDNCALICGNHIMDLCEQANQASATSECTV 70
DB 20 SGTSG-GDKMFSLKKNVAVLWAMDIVDNCALICGNHIMDLCEQANQASATSECTV 75
QY 71 AMGCNHAFFHCISRMLKTRQVCPDLNREWEFOKYG 107
DB 76 VMGCNHSFHNCCMSLWVKQNNRCPLCQGDWVVOIG 112

RESULT 13

US-10-152-156-8
; Sequence 8, Application US/10152156
; Publication No. US20030108947A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGEN
; TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
; FILE REFERENCE: A-68613-6/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/152,156
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,174
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,139

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Page 5

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; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/109,460
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/108,767
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/291,836
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-156-8
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Query Match          46.6%; Score 287; DB 14; Length 113;
Best Local Similarity 49.5%; Pred. No. 4.3e-24;
Matches 48; Conservative 14; Mismatches 31; Indels 4; Gaps 2;
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QY 11 SCNSGAGKRRFEVKKNNAVAMNDIVDNCACIENHMDICICQANQASATSECTV 70
DB 20 SGTSG-GDKMFLKKNPVAMMSWDECDTCACGVQVMDACLRQALN--KQEDCV 75
QY 71 AMGVCHAFHFHCISRWLKTRQVCPDNRNEMEFQKYG 107
DB 76 VMGECHHSFHCMSLWVKNRNCPLQCGDMVQVRIG 112
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RESULT 14
US-10-424-599-242288
; Sequence 242288, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 242288
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(68)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_60814C.1.pep
US-10-424-599-242288
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Query Match          45.8%; Score 282; DB 12; Length 68;
Best Local Similarity 69.1%; Pred. No. 9.1e-24;
Matches 47; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
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QY 24 VKKNAAVAMNDIVDNCACIENHMDICICQANQASATSECTVAMGVCHAFHFHC 83
DB 1 IKNCNADGIVAMNDIVDNCACIENHMDICVDCIANQASSTSECTVARGVNHAIHLHC 60
QY 84 ISRWLXTR 91
DB 61 ICRWVXTR 68
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RESULT 15
US-10-424-599-264079
; Sequence 264079, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 264079
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(40)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80484C.1.pep
US-10-424-599-264079
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Query Match          37.0%; Score 228; DB 12; Length 40;
Best Local Similarity 95.0%; Pred. No. 5.2e-18;
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 69 TVAMGVCHAFHFHCISRWLKTRQVCPDNRNEMEFQKYG 108
DB 1 TVAMGVCHAFHFHCISRWLKTRQVCPDNRNEMEFQKYG 40
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Search completed: March 25, 2004, 09:41:51
Job time : 42 secs
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